

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	629	25.8	457	1	W8137	A delta-6 desatura
2	629	25.8	457	1	W95504	Mortierella alpina
3	620	25.5	457	1	W85121	A delta-6 desatura
4	555	22.8	355	1	W84139	Desaturase enzyme
5	412	16.9	746	1	W84156	Human desaturase e
6	412	16.9	746	1	W85135	A desaturase enzym
7	412	16.9	753	1	W95514	Amino acid sequenc
8	409.5	16.8	448	1	R98455	Borage delta-6-des
9	409.5	16.8	448	1	W67471	Borage delta-6 des
10	409.5	16.8	448	1	R98130	Borage delta-6 des
11	407.5	16.7	446	1	W85122	A delta-6 desatura
12	312.5	12.8	608	1	W84155	Human desaturase e
13	312.5	12.8	608	1	W95134	A desaturase enzym
14	312.5	12.8	615	1	W95513	Amino acid sequenc
15	284.5	11.7	87	1	W84144	Desaturase enzyme
16	259.5	10.7	252	1	W94141	Desaturase enzyme
17	250.5	10.3	555	1	W84154	Human desaturase e
18	250.5	10.3	555	1	W85133	Human desaturase e
19	250.5	10.3	562	1	W95512	A desaturase enzym
20	246.5	10.1	306	1	W84153	Amino acid sequenc
21	246.5	10.1	306	1	W85132	Human desaturase e
22	246.5	10.1	306	1	W95511	A desaturase enzym
23	230.5	9.5	446	1	W85119	Amino acid sequenc
24	230.5	9.5	446	1	W95119	A delta-5 desatura
25	213	8.7	359	1	R34102	Mortierella alpina
26	211	8.7	359	1	R98456	Bacterial delta-6-
27	211	8.7	359	1	R98456	Synechocystis delt
28	211	8.7	365	1	W85124	A delta-6 desatura
29	198	8.1	143	1	W84145	A delta-6 desatura
30	181.5	7.5	211	1	W84151	Desaturase enzyme
31	181.5	7.5	211	1	W85130	Human desaturase e
32	181.5	7.5	218	1	W95509	A desaturase enzym
33	179	6.9	131	1	W84143	Amino acid sequenc
34	168.5	6.9	382	1	W83353	Desaturase enzyme
35	165.5	6.8	379	1	R53699	Vernonia galamnen
36	147.5	6.1	384	1	W24997	Sequence of soybea
37	147.5	6.1	384	1	R34055	Microsomal delta-1
38	147.5	6.1	384	1	W94049	Amino acid sequenc
39	146.5	6.0	384	1	W86155	Amino acid sequenc
39	146.5	6.0	384	1	W86155	Protein sequenc o

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QY 71 PQAANVNEAQRKRLREELIATGMD--ASPLWYSYKISTTLGLGVL-GYFLMVQYQY 127
Db 83 -RDFQVSEVRDYRMAAEFRKLGLENKGVHTLYTAFVAAFLGVLGYLACTSVFAH 141
QY 128 FIGAVLLGMHYQOQWLSHSDICHQTFKRNMMNLVGLVFGNGLQGFVTCWKDRHNAH 187
Db 142 QIAAALLGLWIOSAYIGHDSGHVIMNSKSYNFAQLLSCNCLTGISIAWKKTHNAH 201
QY 188 SATNVQGHDDIDNLPPLANSE-----DDVTRASPISRKLIQFOQY-YFLVICI 235
Db 202 LACNSLDYDPLQHIPVFAVSTKFSLSRFDYRKLTDFDVARFLVSYQHFTYYPVNC 261
QY 236 --LLRFTWCFOCVLTVRSKDRDNQFYRSQYKKEAIGLALHWTALKALFFMPSILTS 293
Db 262 GRNLFOTFLLSKREVDRLNF-----AGILFWT-----PLLVSC 301
QY 294 L-----VFFVSELVGGFGIAIVVF-MNHYPLE-KIGDPVWDGHSVSGQIHTMNIIRG 345
Db 302 LPNWERFFVFTSVTALQHQITLNFHAADVVGPT--GSDWFEKQAAGTIDISCR 359
QY 346 IITDWFEGGLNYQIEHLLWTLPHRNTAVSYQVEQLCQKHNLPYRNLPHLEGVLILRY 405
Db 360 SYMD-PFGGLQFOLEHLLFRLPRCHPRKVPFVVQVELCKRKLXLPYRSMSWFEANVLT 418
QY 406 LAVFARMA 413
Db 419 LKTAAYQA 426

RESULT 11
QY500 PRELIMINARY; PRT; 445 AA.
AC QY500;
DT 01-NOV-1999 (TEMBLrel. 12, Created)
DT 01-NOV-1999 (TEMBLrel. 12, Last sequence update)
DE DELTA-6 FATTY ACID DESATURASE.
GN CYB5RP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA LI W., METZGER M.L., CASKEY C.T., PETRUKHIN K.;
RT "Human retina-specific delta 6 fatty acid desaturase.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF134404; AAD31282.1; -.
SQ SEQUENCE 445 AA; 51145 MW; 7D975F81 CRC32;

Query Match 19.4%; Score 443.5; DB 4; Length 445;
Best Local Similarity 29.8%; Pred. No. 3.7e-33;
Matches 123; Conservative 61; Mismatches 160; Indels 69; Gaps 14;

QY 11 LQIMEOTYDVSAMVNFPHGGAETIENYQGRDATDAFVMVH----FOAEKDLKRMKINP 66
Db 39 LVIERVYDISWAQRHGGSLRUGHGHAEADATDAFRAHODUNFVRKFLQPLLIGELAP 98
QY 67 SFELPPQAAVNEAQ--EDFRKRLREELIATGMDASPLWYSYKISTTLGLGVLGYFLMVQY 124
Db 99 --EESQDGLNLAQVDFRALHQAEDMKLFDASTFFAFLGLHILAMEVLAWLL----153
QY 125 QMYFTG-----AVLLGMHYQOQWLSHSDICHQTFKRNMMNLVGLVFGNGLQGF 175
Db 153 -IYLLGPGWVPSALAFILASQAQSWCLQHDLGHASIFKSWNNHVAQKFMVQGLKGF 211
QY 176 VTCWKDRHNAHSATNVQGHDDIDNLPPLANSEDDVTRASPISRKLIQFOQ--YFLV- 233
Db 212 AHWNFRHFQHAKNPINFHKDDVTVAPVLLGESSVEYKKRRYLPYNQOHLFEFLG 271
QY 233 --ICILRFIWCFOCVLTVRSKDRDNQFYRSQYKKEAIGLALHWTALKALFFMPSILTS 293

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Db 272 PPLTLTVNF-----EVENLAY-----MLVCMQWADLLWAASTYARFEL 309
QY 284 FFMPSI-LTSLVFFVS-ELVGGFGIAIVVFMMHYPLEKIGDPVWDGH----GFSVGQIH 337
Db 310 SYLPFYGPVGLVFFVAVRVLESHWFVWITQMNHIKPE-----IGHEKRDWVSSOLA 362
QY 338 ETNNIRGILTDNFFGGLNQIEHLLWTLPHRNTAVSYQVEQLCQKHNLPY 390
Db 363 ATCNVESLFTNWFSGHLNFQIEHLLFPRMHRNYSRVAPLVKSLCAKHLGY 415

RESULT 12
QY500 PRELIMINARY; PRT; 448 AA.
AC QY500;
DT 01-JUL-1997 (TEMBLrel. 04, Created)
DT 01-JUL-1997 (TEMBLrel. 04, Last sequence update)
DE DELTA 6 DESATURASE.
OS Borago officinalis (Bourrache).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Asteridae; euasterids I; unclassified euasterids I;
OC Boraginaceae; Borago.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97268723.
RA SAYANOVA O., SMITH M.A., LAPINSKAS P.A., STOBART K., DOBSON G.;
RA CHRISTIE W.W., SHEWRY P.R., NAPIER J.A.;
RT "Expression of a borago desaturase cDNA containing an N-terminal
RT cytochrome b5 domain results in the accumulation of high levels of
RT delta6-desaturated fatty acids in transgenic tobacco.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:4211-4216(1997).
DR EMBL; U79010; AAC49700.1; -.
DR MENDEL; 15845; Borof;2419;15845.
DR PFAM; PF00173; hemeL; 1.
SQ SEQUENCE 448 AA; 51634 MW; 539A4EDA CRC32;

Query Match 19.2%; Score 437.5; DB 10; Length 448;
Best Local Similarity 29.6%; Pred. No. 1.4e-32;
Matches 120; Conservative 65; Mismatches 171; Indels 49; Gaps 12;

QY 11 LQIMEOTYDVSAMVNFPHGGAETIENYQGRDATDAFVMVHFOEAFDLKRMKINPSFEL 70
Db 25 ISIQKAYDVSQWYKDPHGGSPFLKSLAQEVTDAFVAFHASTW---KNLDFFTGYL 81
QY 71 PQAANVNEAQRKRLREELIATGMDA-----SPLWYSYKISTTLGLGVLGYFLMVQY 124
Db 82 -KDYSEVSEVKDYRKLVTFESKMGULYDKKGHMFATLCE---IAMLFAMSVYGVLFCEGV 137
QY 125 QMYFTGAVLLGMHYQOQWLSHSDICHQTFKRNMMNLVGLVFGNGLQGFVTCWKDRHN 184
Db 138 LVHFLSGCLMGLFWIQSGWIGHDAGHYVMYVSDSRNKNKFGIFAANCLSGISIGWKNHN 197
QY 185 AHSATNVQGHDDIDNLPPLANS-----EDVTRASPISRKLIQFOQYFLV 232
Db 198 AHHAACNSLEYDPLQYIPFLVVSFKFGSLASHFEYKRLTFDS-LSREFVSVQHWTFYP 256
QY 233 ICILRFIWCFOCVLTVRSKDRDNQFYRSQYKKEAIGLALHWTALKALFFMPSILTS 292
Db 257 IWCARLNMYVQSLI---MLLTRNVSYRA-----HELGLCVFSIYPLVSC 302
QY 293 L-----LVFFVSELVGGFGIAIVVF-MNHYPLE-KIGDPVWDGHSVSGQIHTMNIIRG 345
Db 303 LPNWERIMFVIASLVTGMOQVQVSLNHFSSSVVVGKP--KGNWFEKQDTGDLDISCP 360
QY 346 IITDWFEGGLNQIEHLLWTLPHRNTAVSYQVEQLCQKHNLPY 390
Db 361 PMWDFHFGLOQIEHLLFPPKPRCNKRKISPYVIELCKKHNLPY 405

RESULT 13

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RC STRAIN-CV. DRAKKAR; TISSUE-RIPENING EMBRYOS;
RX MEDLINE; 99003197.
RA SHERLING P., ZAHRINGER U., HEINZ E.;
RT "A sphingolipid desaturase from higher plant
cytochrome b5 fusion protein.";
RL J. Biol. Chem. 273:28590-28596(1998).
DR EMBL; AJ224160; CAA11857.1; -.
DR HSPG; P00173; IAGA.
DR MENDEL; 34704; Brana.2419:34704.
SQ SEQUENCE 449 AA; 51490 MW; F9BB69EE CRC3

Query Match	21.88;	Score 498;	DB 10;	Length 449;
Best Local Similarity	32.08;	Pred. No. 3.2e-38;		
Matches 135; Conservative	72;	Mismatches 177;	Indels 38;	Gaps 13;
QY	11	LQMLEQYDVDSAWNFHPGGAEITENTQGRDATDAFVMVHFQEAFLDKLRKMPKINPSEL	70	
DB	26	ISIQKYVDVSHVWKSPHGGAAALNLAGQDVTDAFIAYHPGTAW--RHLNHLNGXHV	82	
QY	71	PPQAAVNEAQEDFRKLREELIATGMFAS----PLWYSYKITTIGLGLVGLYFELMVQYQY	127	
DB	83	KDH-HVSDVSRDYRRLAAEFESKRGLEFKKHWTLYTLTCVAAMLAAYVYGVVACTSIWAH	141	
QY	128	FIGAVILGMHYQWGNLSHDICHQTFKRNWNINLVLFVNGNLQGFVSVCWKDRHNAHH	187	
DB	142	LISAVILGLLWQIAYVGHDSGHYNTSTKPCNKLVQLLSGNCITGTSIAWKWKTHNAHH	201	
QY	188	SATVNOGHDPDIDNLPPLAWSE--DDVTRA-----SPISRKLIQFOQY-YFLVVICI	235	
DB	202	ISCSNLSDHPDLQHPVLAVSNKFKSMTSREYGRKLTDFDLAREFLISYQHWSEVPINCV	261	
QY	236	--LRLFTWCFOCVLTVRSCLKDRDNOFYRSQYKKEAIGLALHWLTKALPHLEFPMFSILSL	293	
DB	262	GRINLFQITLTLFLFSRRYVDP-----ALNIAGILVFETWTFPLL-VSFLPNWQERI	311	
QY	294	LVFFVSELVGGFGTAIVVF-MNHVPLEKIGDPVWDGHGFSVGOIHETWNIRRGITTDWFF	352	
DB	312	IFVFLSMAY--TAQHVOFCNLHFAADYYVTGPP-NGNDWFEPKQATGTLIDISCRSYMDFEF	368	
QY	353	GGLNYQIEHHLWPTLPRHNLTAVSQVBOLCCKHNLPYRNPLPHEGLVILLRYL---AVF	409	
DB	369	GGIOLEHHLUFLPRLPRCHLGRSVVQELCKKHNLPYRSLSWEEANYTLTLRKAAVO	428	

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. . .
DR HSP; P00171; LWDB.
DR MENDEL; 34619; Arath;2419;34619.
SQ SEQUENCE 449 AA; 51675 MW; 36C26D4D CRC32;
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Query Match          21.4%; Score 488.5; DB 10; Length 449;
Best Local Similarity 30.5%; Pred.No. 2.5e-37;
Matches 131; Conservative 67; Mismatches 179; Indels 53; Gaps
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Qy      11 LQLMEQTIDYSAVNFHPGGAETIENYGQRDATAPFVMHFOEAFDKLRMPKINPSFEEL 70
       :   |::|:|:|:|:|:|:~::~|||:~::|:~::|:~::|:~::|:~::|:~::|:~::|:~::
Db     26 IATQGKYNYNSDIKTTHPGGDVTILNLVGQDYTDPIAEFGCTAWHHLDH---LFTGYHI 82

Qy      71 PPQAANVEAODEFRKLREELIATGMFD--ASPLWYSYKIISTTLGLGVL-GYFLMVOYQM 127
       :   |::|:~::|:~::|:~::|:~::|:~::|:~::|:~::|:~::|:~::|:~::|:~::
Db    83 -RDFQSEVSERDYRMVAEFRLKLGLEPENKGHVLTLYLAFAAMFLGVLVGLACTSVFAH 141

Qy     128 FIGAVLLGHMYQQMGWLSDHCCHHTFKNRNNNVLGLVFNGLOGFSVTCWKDRHNNAH 187
       |||:~::|:~::|:~::|:~::|:~::|:~::|:~::|:~::|:~::|:~::|:~::|:~::
Db   142 QIAAAALLGLNWISAYIGHDSGHVIMSNKSYNRFAGLLSGNCLTGISIAMKKWTNHNAH 201

Qy     188 SATNVQHSHDDPDLNLPLAWSE-----DDVTRASPISRKLIOFOOY-YFLVICI 235
       :   |::|:~::|:~::|:~::|:~::|:~::|:~::|:~::|:~::|:~::|:~::|:~::
Db   202 LANSLDYDPLOHQIPVFAVSTWFSSLSIRFYDRKLTDPVARFLVSIQHYTYPPVMCF 261

Qy     236 --LLREFTWFCQCULTVRSKDRDNQRYRSQYKKEAIGALHWTKALF-----HLF 284
       :   |:~::|:~::|:~::|:~::|:~::|:~::|:~::|:~::|:~::|:~::|:~::|:~::
Db   262 GRINFLOTELLFSKNREVPDRALN-----AGILVFWTFPLLVSCLPNPMPEFF 312

Qy     285 FMSILTSLVVFPSELVGFGFIIVFMNHPLE-KIGDPVDWGHSFGSVOIHETMNIR 343
       |:~::|:~::|:~::|:~::|:~::|:~::|:~::|:~::|:~::|:~::|:~::|:~::
Db   313 F---VFTSFVTALQH-----IIOTLNHFAADYYVGPPT--GSDWEKOAGAATIDIS 359

Qy     344 RGIITDWFFGGLYNQIEHHLPRTLPRHNTAVSYQEOLCQKHNPYPRNPLEHGILLV 403
       ||||~::|:~::|:~::|:~::|:~::|:~::|:~::|:~::|:~::|:~::|:~::|:~::
Db   360 CRSYMDFWFFGLGFQLEHHLFRLPCRLRKRVSPVVOELCKKHNLPLYRSMSSFANVLTI 419

Qy     404 RYLAVAFARMA 413
       |_____|_____
Db   420 NTLKTAAYQA 429

RESULT 10
Q9ZtZ9 PRELIMINARY; PRG: 446 AA.
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ID Q9ZTz9 PRELIMINARY; PRG: 446 AA.
AC Q9ZTz9;
DT 01-MAY-1999 (TEMBREL. 10, Created)
DT 01-MAY-1999 (TEMBREL. 10, Last sequence update)
DT 01-NOV-1999 (TEMBREL. 12, Last annotation update)
DE FATY ACID DESATURASE/CYTROCHROME B5 FUSION PROTEIN.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; eudicotyledons; Spermatophyta; Magnoliophyta; euclcotyledons; core eucotics; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsiis.
CN [1]
RC SEQUENCE FROM N.A.
RA TISSUE=DEVELOPING SILIQUES;
RC SAYANOVA O., STOBART A.K.; SNEYDER P.R.; NAPIER J.A.;
RL Submitted (Apr-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF001394; AACD00895.1; -.
DR HSP; P00171; IWDB.
DR MENDEL; 35700; Arath;2419;35700.
SQ SEQUENCE 446 AA; 51247 MW; 18C9FF05 CRC32;
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Query Match      19.7%   Score 449;   DB 10;   Length 445;
Best Local Similarity 29.%;   Pred. No. 1.le-38;
Matches 127; Conservative 68; Mismatches 181; Indels 52; Gaps 14;
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Qy 182 RHNAHSTNTVGGHDPPDINDLPLPLAWSDDVDTRASPIS--RKLIQFOQYFVLCILLRF 239
Db 207 QHNVHHAATNTVGRGDLDLVPFYATVAEHLNNYSODSWMTLFRWQHVVHTMPLFLRL 266
Qy 240 TWFCOVLTVRSLRDRNQFVRSQYKKEATGLAHHTLKALFLHPMPSLTSLLYFFVS 299
Db 267 SWLQSIIIFVSOMTHYDYDYNRTAIVYEQVLSUHWAW-SLGQLYFLPDWSTRIMEFLVS 325
Qy 300 ELVGGFGIAIVFMNHYPLEKIGDVPVMDGHGVSQVGHETMNIIRRGIIIDWFEGGLNYOI 359
Db 326 HLVGFGLLSHVVTNNHYSVEKFASSNIMSNYACLIQMTTRNMPGGRFDLWGLGGLNYOI 385
Qy 360 EHLHWPTLPRLNLTAVSYQVEQLCKINLPY 390
Db 386 EHLHFTPMRNLNTVMPLYKFAAANGLPY 416

RESULT 2
Q94044 PRELIMINARY; PRT; 454 AA.
ID Q94044
AC Q94044;
DT 01-FEB-1997 (Tremblrel. 02, Created)
DT 01-FEB-1997 (Tremblrel. 02, Last sequence update)
DE T13F2.1 PROTEIN.
DE T13F2.1
GN Cnaenorhabditis elegans.
OS Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
OC Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
[1]
RN RABDITINAE
RA SWINBURNE J.;
RA SEQUENCE FROM N.A.
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 94150718.
RA WILSON R., AINSOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORFIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIEKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA SHALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans".
RL Nature 368:32-38(1994).
DR EMBL: Z81122; CAB0332.1;
SQ SEQUENCE 454 AA; 53160 MW; D7FD13FA CRC32;

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QY	233	ICILRLRFWCFCQCVLTVRSKLDRDNQYFYSQYKKEALGHALHTWLKALFLHFLFMP	SILTS	292
Db	267	MLPFLRLSWLQSIIFVSQMPHTHYDYRTATAYEQVGLSHWAW-SLQGLYFLPDW	STR	325
QY	293	LLVFEVSELVGGGICIAIVFMNHYPLEKIGDPVWDGHSVSGIYHETMNIIRGIIITD	WFF	352
Db	326	IMFELVSLHVGGLSHVWTFNHYSVBEKFLSSNIMSNVACLIQIMTTRNNRPGREF	DWLW	385
QY	353	GGLNAVQIEHHLWPTLPRHNLTAYSVQVEQLCQKHNL	LPY	390
Db	386	GGLNYQIEHHLFTPRHNLNTVNP	LVKFEFAAANG	LPY 423
RESULT	3			
O61388		PRELIMINARY;	PRF;	443 AA.
ID	O61388			
AC	O61388;			
DT	01-AUG-1998 (TEMBLrel. 07, Created)			
DT	01-AUG-1998 (TEMBLrel. 07, Last sequence update)			
DT	01-NOV-1998 (TEMBLrel. 08, Last annotation update)			
DE	DELTA6-FATTY-ACID-DESATURASE.			
OS	Caenorhabditis elegans.			
OC	Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;			
CC	Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 97368723.			
RA	SAYANOVA O., SMITH M.A., LAPINSKAS P., STOBART A.K., DOBSON G.,			
RA	CHRISTIE W.W., SHEWRY P.R., NAPIER J.A.;			
RT	"Expression of a borage desaturase cDNA containing an N-terminal			
RT	cytochrome b5 domain results in the accumulation of high levels of			
RT	delta6-desaturated fatty acids in transgenic tobacco.";			
FL	Proc. Natl. Acad. Sci. U.S.A. 94:4211-4216(1997).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 98149727.			
RA	NAPIER J.A., HEY S.J., LACEY D.J., SHEWRY P.R.;			
RT	"Identification of a Caenorhabditis elegans Delta6-fatty-acid-			
RT	desaturase by heterologous expression in Saccharomyces cerevisiae.";			
FL	Biochem J. 330:0-0(0).			
DR	EMBL; AF031477; AAC15586.1; "			
SQ	SEQUENCE 443 AA; 51740 MW; EE44468D			CRG32;

Query Match 27.4%; Score 625; DB 5; Length 454;
Best Local Similarity 36.4%; pred. No. 5.2e-50;
Matches 145; Conservative 64; Mismatches 151; Indels 38; Gaps 10;

Best Local Similarity 20.7%; Pred. No. 0.0067;
Matches 82; Conservative 65; Mismatches 153; Indels 96; Gaps 25;

QY 29 GGAETIENQGRDATDAFVWVHFOEAFDKLRMPKINPSEFEL-----PPQAAVNEAQE 81
DB 2 GSLIGSEIYD-----KNSFEMEPEF--FD-----PSAPPPERLAEIRNVIPKHCVKDPDLR 50

QY 82 DFRKREELIATGMFASPLWYSKISTTGLGV--LGYFLWVQYOMYFVIGAVLLGHYQO 140
DB 51 SLISVVRDVF-----VATLIGIAHLDSNLF--YPLW---AIOGMFWA 91

QY 141 MGWLSHDICHQHTKRN--WNNLVGVFNGL-----OGFSVTCWKDRHNAHHSATNVQGH 195
DB 92 IFVLGHD-CGHSFSDSOLLNNVGVHLSAILVPYHG-----WRISHKTHH-----QNH 140

QY 196 -DPDIDNPLAWSEDDVTRASPISRKLIQFOQYFVLCILLRF-IWCFQCVLTVRSLK 253
DB 141 GNVTDE-----SW-----VPMPEKLYNKVGYSTKFLYKIPFPPLAIPMYLMKRSFG 188

QY 254 DRDNQF-----YRSQYKKEAIGLALHWTLKALHFFMPSI--LTSLLVFFVSELVGGF 305
DB 189 KGSHPENPSDLFQPHRKVYVSTLCWTYMAALLYLCTAFGLQWLFKYGAPYLIFVM 248

QY 306 GIAVFMNHPLEKIGDPVMDGHGFSVGOIHETMNRIGIIT---DW-PFGGLNVOIE- 361
DB 249 WLDFVYTLHHGGEK-KLPYRGKEWSY-----LRGLTIVDRDYGLEFNHHDIGT 299

QY 361 ---HHLWPTLPRNLTAVSYQVEQLCKHNLPRNP 393
DB 300 HVTHLFPQIPHLYHLREATKAAPVGLGY---YREP 332

RESULT 14
FD3C-SOYBN STANDARD; PRT; 453 AA.

AC P48621;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR (EC 1.14.99.-).
GN PAD7.

OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae;
OC Glycine.
[1]

RN SEQUENCE FROM N.A.
RC TISSUE-SEED;
RX MEDLINE; 94302147.
RA YADAV N.S., WIERZBICKI A., AEGERTER M., CASTER C.S., PEREZ-GRAU L.,
RA KINNEY A.J., HITZ W.D., BOOTH J.R. JR., SCHWEIGER B., STECCA K.L.,
RA ALLEN S.M., BLACKWELL M., REITER R.S., CARLSON T.J., RUSSELL S.H.,
RA FELDAMANN K.A., PIERCE J., BROWSE J.;
RT "Cloning of higher plant omega-3 fatty acid desaturases.";
RL Plant Physiol. 103:467-476(1993).

CC -1- FUNCTION: CHLOROPLAST OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY
CC ACIDS, IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT
CC TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/ OR BE INVOLVED IN METAL ION-BINDING.
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
CC

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CC CC EMBL; L22965; AAA61776.1; -
DR PIR; J02339; J02339.
DR PFAM; PF00487; FA_desaturase; 1.
KW Oxidoreductase; Fatty acid biosynthesis; Chloroplast; Membrane;
KW Transit peptide.
FT TRANSIT 1 ?
FT CHAIN 1 ?
FT CHAIN 2 453
FT CHAIN 3 453
FT DOMAIN 171 175
FT DOMAIN 207 211
FT DOMAIN 374 378
FT SEQUENCE 453 AA; 51362 MW; E4314F1B CRC32;

Query Match 5.1%; Score 117; DB 1; Length 453;
Best Local Similarity 20.3%; Pred. No. 0.01;
Matches 92; Conservative 72; Mismatches 150; Indels 140; Gaps 25;

QY 7 ALSPLQIME--QTYDSAVNPHFGGAETIENQGRDATDAFVWVHFOEAFDKL----- 59
DB 26 ALSSTSRVEFLDTNKVVGPKFQPLRCNLRRNWLKVSAPLRVASIEEERQKSYDLTNGT 85

QY 59 -----KMPKINPSEFELPP-----QAAVNE---AQEDERKL-----REELIATGMFAS 99
DB 86 NGVEHEKLPEDPG--APPPFNLAIRAAIPKHCWKOPWRSYVYVVRVIAVFGLAANA 143

QY 100 -----PLMYSYKISTTGLGVGLVFLWVQYOMYFVIGAVLLGHYQOGLSHDICH 150
DB 144 AYLNNLVWPLYWRAQ-----GTFWALFV-----LGHD-CG 174

QY 151 HQTFRNRN--WNNLVGVFNGL-----OGFSVTCWKDRHNAHHSATNVQGHDPIDNLPPL 205
DB 175 HGSFSNNSKLSVGVHLLHSSILVPYHG-----WRISHRTHQH-----HGAENDESHP 226

QY 206 A-----WSEDVTRASPISRKLIQFOQYFVLCILLRF-----IWCFOCVLTVRSLK--- 254
DB 227 PEKLFSLDTVTR-----MURFTAPFPPLAIPVYLFSSRPSKGT 265

QY 254 ---DRDNQFVRSQYKKEAIGLALHWT--LKALHFLFFMPSILTSLLVFFVSELVGGFGIA 308
DB 266 SHEDPSDLFVPERKDVITSTACWAAMLGLLVGLGVVMPQIQLKLYGVYVIFVMWLD 325

QY 309 IYVFMNHPLE-KIGDPVMDGHGFSVGOIHETMNRIGIIT-DWFFGGLN-----YQI 359
DB 326 LVTYLHHGHGHEKDL--PWYRGKEWSY-----LRGLTIVDRDYGWINNIHHDIGTHV 375

QY 360 EHLWPTLPRNLTAVSYQVEQLCKHNLPRNP 393
DB 376 IHLFPQIPHLYHLVEATEAKAPVGLGY---YREP 406

RESULT 15
FD3C-SPIOL STANDARD; PRT; 447 AA.

AC F48629;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE OMEGA-6 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR (EC 1.14.99.-).
GN PAD6.

OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Caryophyllales; Caryophyllaceae; Chenopodiaceae;
OC Spinacia.
[1]

RN SEQUENCE FROM N.A., AND SEQUENCE OF 66-78.
RC STRAIN-CV. SUBITO; TISSUE-LEAF;
RX MEDLINE; 9503604.
RA SCHMIDT H., DRUSSELHAUS T., BUCK F., HEINZ E.;
RT "Purification and PCR-based cDNA cloning of a plastidial n-6
RT desaturase.";

```

RESULT 12
FD32_BRANA STANDARD; PRT; 383 AA.
AC P48624;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE (VERSION 2).
DE OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (EC 1.14.99.-)
GN FAD3.
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
OC Brassica.
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE: 93088059.
RA ARONDEL V., LEMIEUX B., HWANG I., GIBSON S., GOODMAN H.M.,
RA SOMERVILLE C.R.;
RT "Map-based cloning of a gene controlling omega-3 fatty acid
RT desaturation in Arabidopsis.";
RL Science 258:1353-1355(1992).
CC -1- FUNCTION: ER (MICROSOMAL) OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS,
CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
CC PHOSPHOLIPIDS.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/ OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: L01418; AAA32994.1; -.
CC PFAM: PF00487; FA_desaturase; 1.
CC Oxidoreductase; Fatty acid biosynthesis; Endoplasmic reticulum;
CC Transmembrane.
CC TRANSMEM 53 73 POTENTIAL.
CC TRANSMEM 210 230 POTENTIAL.
CC TRANSMEM 234 254 POTENTIAL.
CC TRANSMEM 98 102 HISTIDINE BOX 1.
CC DOMAIN 134 138 HISTIDINE BOX 2.
CC DOMAIN 301 305 HISTIDINE BOX 3.
CC SEQUENCE 383 AA; 43936 MW; F39A978B CRC32;

Query Match 5.3%; Score 120; DB 1; Length 383;
Best Local Similarity 20.7%; Pred. No. 0.0046;
Matches 78; Conservative 66; Mismatches 136; Indels 96; Gaps 21;

QY 52 QEAFDKLKPKNPNSFEL-----PPQAAVNEAQEDFRKLREELIATGMFD 97
DB 20 EGGD-----PSAQPFPKIGDIRAAIPKHCWKSPLRMSYVTRDIFAAALAAVAAYFD 74
QY 98 ASPLWYSKISTTLGLGVGLYLMVQYQMYFICAVLLGHMYQGMWLSHDICHHTQFKNR 157
DB 75 SNFLPLVYVAQ---GTLFWAIFV-----LGHD-CGHGFSFD- 108
QY 158 NNNNLVGLVFGNGLOQFSVT---CWKDRHNAHSATNVQGHDPDIDNPLPLAWSEDDVTR 214
DB 108 --IPLLSVVGHILHSFILVPYHGWIRSHRTHQN---HGVENDESQWVPL---PEKLYK 159

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QY 215 ASPISRKLIQFQYYFLVICILLRFTWCFOCVLTVRSKLDKDNQF---YRSQY-----KKEA 268
DB 160 NLFPHSTRMLR---YTVPLPML-----AYPIYLWYRSPGKEGSHFNYPYSSLFAPSERKLI 210
QY 269 IGLALHWT--LKALFLHFLFEMPSILTSLVFFSVSELVGFGIAIVVENHYPYLP-EKIGDPV 325
DB 211 ATSTTCSIMLAIVLSFLVDPVTVLKVIYGVPIYIFVMDLDAVTYLHHGHGDEKL--PW 268
QY 326 WDGHGFSVGVIHETMNIIRGIIT---DW-FFGLNYQIE---HHLWPTLPRLHNLTAHSV 377
DB 269 YRGKEWSY-----LRGGLTIDRDYGIFFNNIHHIDGTHVIHHLFPQIPHYHLVDATR 320
QY 378 QVQLCOCKHNLPRNP 393
DB 321 AAKHVLGRY---YREP 333

RESULT 13
FD3E_TOBAC STANDARD; PRT; 379 AA.
AC P48626;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (EC 1.14.99.-)
GN FAD3.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Asteridae; euasterids I; Solanales; Solanaceae;
OC Nicotiana.
RN [1]
RN SEQUENCE FROM N.A.
RX STRAIN-CV. SRI; TISSUE-LEAF;
RX MEDLINE: 95011632.
RA HAMADA T., KODAMA H., NISHIMURA M., IBA K.;
RT "Cloning of a cDNA encoding tobacco omega-3 fatty acid desaturase.";
RL Gene 147:293-294(1994).
CC -1- FUNCTION: ER (MICROSOMAL) OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS,
CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
CC PHOSPHOLIPIDS.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/ OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: D26509; BAA05515.1; -.
CC PFAM: PF00487; FA_desaturase; 1.
CC Oxidoreductase; Fatty acid biosynthesis; Endoplasmic reticulum;
CC Transmembrane.
CC TRANSMEM 52 72 POTENTIAL.
CC TRANSMEM 213 233 POTENTIAL.
CC TRANSMEM 236 256 POTENTIAL.
CC DOMAIN 97 101 HISTIDINE BOX 1.
CC DOMAIN 133 137 HISTIDINE BOX 2.
CC DOMAIN 300 304 HISTIDINE BOX 3.
CC SEQUENCE 379 AA; 44149 MW; C237E46D CRC32;

Query Match 5.2%; Score 118; DB 1; Length 379;

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DR	EMBL; U25817; AAA70334.1; -.
DR	PFAM; PF00487; FA_desaturase; 1.
DR	Oxido-reductase; Fatty acid biosynthesis; Chloroplast; Membrane;
FT	Transit peptide.
FT	TRANSIT 1 ? CHLOROPLAST (POTENTIAL).
FT	CHAIN ? 447 OMEGA-3 FATTY ACID DESATURASE.
FT	DOMAIN 167 171 HISTIDINE BOX 1.
FT	DOMAIN 203 207 HISTIDINE BOX 2.
FT	DOMAIN 370 374 HISTIDINE BOX 3.
SQ	SEQUENCE 447 AA; 51116 MW; 67B2C46B CRC32;

Query Match 5.6%; Score 127; DB 1; Length 447;
Best Local Similarity 22.1%; Pred. No. 0.0014;
Matches 99; Conservative 71; Mismatches 155; Indels 122; Gaps 29;

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QY 1 MKSRQAL---SPQLMEQTYDVSAWNFHPGGAETIENYQGRDATDAFYVMHFQEAQDK 57
55 LREKNALRYSAPLRYLOV-----EEEEENVEGE-----RVINGGEED- 94
Db

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OV 58 LKRM PKINPSELPPOAAVNEAOEDERKLBEEI.TATGMEDASPI.WYSV.---KTSTTTC 112

Db 94 ----PGAPPPPEKL-----SDIR-----EAI PKHCWVKDP--WRSMGYVVRDVA VVFG 134

QY 113 L-GVLGYF-LMVQYQMYFIGAVLLGMHYQQMGW----LSHDICHHQTFKN-RNWNNLVGL 165

Db 135 LAATAAYFNNVWPLYWEA-----QSTMFWALEVLGHD-CGHGSEFNDPKLNSVVGH 186

QY 166 VFGNGL- - - - QGFSVTCWKDRHNAHHSATNVQGHDPDIDNLPPLAWSEDDVTRASPISRK 221

Db 187 ILHSSILVPYHG----WRISHRTHQN---HGHWENDESWHPLS---EKIYKNLDTATK 235

QY ZZZ LIQFQIIFLVICILRFLWCFCVLTVRSLKDR-----DNQFYRSQYKKEAIGLALHW 275

00 250 NAME 10FFFFE6A1F4 1DMS - ASFKQ938EHFDSDFVFNEKNDV11SIVCW 280

Year	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1990	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100											

Qv 333 VCOIUEFMNIBDCTIE - DUREDCI N - F - E - VOTBUNT NDEY DBUNT EBNVCKUINBOY CO 334

DB 345 Y-----L BGGITTI DBRYCWINNIHHDICTHVIHHI EDOIDPHVHI I EATEAAKDVIC 306

QY 385 KHNLPYRN-----PLPHEGLVILLRYL 406

Db 397 KY---YREPKKSAPLFFHLLGDLTRSL 420

FD3E_PHAU
TO FD3E PHAMU
STANDARD
DDE
200 2

AC P32291;
DT 01-OCT-1993 (Re) 27 Created)

DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)

DE OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (EC 1.14.99.-)
DE (INDOLE-3-ACETIC ACID INDUCED PROTEIN ARG1).

OS Phaseolus aureus (Mung bean) (Vigna radiata).

euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;

OC
PV
Vigna.
(1)

RP SEQUENCE FROM N.A.
RC TISSUE=HYPOCOTYL.

```

Db 79 GPLSER-----GMAI---YNAVO-----GCILTV-----WVIAHECGHAFSDYQLL 118
QY 160 NNLVGLVFGNGL--QGFSVTCWDRHNAHSATNVQGHDPDIDNLPPLAWSEDDVTRASP 217
Db 119 DIIVGLILHSALLVPYFS---WKYSRRHHSNTG-----SLERDEV--FVP 159
QY 218 ISRKLIOFOQYYP-----LVICILLRFTWCQCCLTVRS-----LKD 254
Db 160 KOKSCIKWYSKYLNNPGRVLTAVTLTGLWPLYLALNVSGRYPDFACHYDYPGIYS 219
QY 255 RON-QYRSQYKKEALGLHWLTKALFLHFFMPSILTSLLVFFVSELVCGFGIAIVFEM 313
Db 220 RERLQIYIS---DAGVLAV---VYGLFRMAKAGLAWVYCVYGVPLLVYNGFLVLITFL 272
QY 314 NH-YP-LEKIGDPVMDGHGFSVGOIHETMNRIRGITDWFEGGLNQIEHHLWPTLPRHN 371
Db 273 QHTHPALPHYTSEWD---WLRGAL-ATVDRDYGILNKVFHNITDTHVAHHLFSTMPHYH 328
QY 372 LTAVSYQVEQLCOKHNLPR 391
Db 329 AMEATKAIRKILGEY---YR 345

RESULT 7
FD6E-ARATH STANDARD; PRT; 383 AA.
AC P46313.
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE OMEGA-6 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (EC 1.14.99.-)
DE (DELTA-12 DESATURASE).
GN FAD2
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
OC Arabidopsis.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 94176997.
RA OKULEY J., LIGHTNER J., FELDMANN K.A., YADAV N., LARK E., BROWSE J.;
RT "Arabidopsis FAD2 gene encodes the enzyme that is essential for
RT polyunsaturated lipid synthesis.";
RL Plant Cell 6:147-158(1994).
CC -!- FUNCTION: ER (MICROSOMAL) OMEGA-6 FATTY ACID DESATURASE INTRODUCES
CC THE SECOND DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS,
CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
CC PHOSPHOLIPIDS.
CC -!- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
CC -!- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/ OR BE INVOLVED IN METAL ION BINDING.
CC -!- SIMILARITY: TO OTHER PLANT ER OMEGA-6 FATTY ACID DESATURASES.
CC -----
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CC -----
CC EMBL; L26296; AAA32782.1; -.
CC PFAM; PF00487; FA_desaturase; 2.
KW Oxidoreductase; Fatty acid biosynthesis; Endoplasmic reticulum;
Transmembrane.
FT TRANSMEM 56 76 POTENTIAL.
FT TRANSMEM 117 137 POTENTIAL.
FT TRANSMEM 179 199 POTENTIAL.

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FT TRANSMEM 225 245 POTENTIAL.
FT TRANSMEM 232 272 POTENTIAL.
FT DOMAIN 105 109 HISTIDINE BOX 1.
FT DOMAIN 141 145 HISTIDINE BOX 2.
FT DOMAIN 315 319 HISTIDINE BOX 3.
SQ SEQUENCE 383 AA; 44047 MW; 192C3433 CRC32;

Query Match 5.9%; Score 134; DB 1; Length 383;
Best Local Similarity 20.3%; Pred. No. 0.00029;
Matches 74; Conservative 52; Mismatches 135; Indels 104; Gaps 19;

QY 56 DKLRMPKINPSE-----LPPQAAVNEAQEDFKRLREELATGMFDASPLWYSKIS 108
Db 19 DTKRVPCEKPFESVGDLLKKAIPPHCFKRSFSLISDIISACF-----YYVA 70
QY 109 TLLGLGLVGLVFMVQYFYI-----GAVLLGMHVQOMGWLSDHICHHOTFKNRNW 159
Db 71 T-----NYFSLLPQPLSYLAWPLYWACOGCVLTGI-----WVIAHECGHAFSDYQW 117
QY 160 -NNLVGLVFGNGL--QGFSVTCWDRHNAHSATNVQGHDPDIDNLPPLAWSEDDVTRAS 216
Db 118 LDDTVGLIFHSFLLPYFS---WKYSRRHHSNTG-----SLERDEV--FV 158
QY 217 PISRKLIQFOQYYP-----LVICILLRFT--WCFQCCLTVRS-----LK 253
Db 159 PKOKSAIKWYKYLNNPGRVLTAVTLTGLWPLYLALNVSGRYPDFACHYDYPNAPIYN 218
QY 254 DRDN-QYRSQYKKEAIGLALH-----WTLKALFLHFFMPSILTSLLVFFVSELVCGFGI 307
Db 219 DRERLQIYLSDAGILAVCGGLYRYAAAGWASMICLYGVPLL-----IVNAFLV 267
QY 308 AIYVFMNHY-P-LEKIGDPVMDGHGFSVGOIHETMNRIRGITDWFEGGLNQIEHHLWPT 366
Db 268 LITVLQHTPSLPHYDSEWD---WLRGAL-ATVDRDYGILNKVFHNITDTHVAHHLFST 323
QY 367 LPRHN 371
Db 324 MPHYN 328

RESULT 8
FD3C-SESIN STANDARD; PRT; 447 AA.
AC P48620;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR (EC 1.14.99.-).
GN FAD7.
OS Sesamum indicum (Oriental sesame) (Gingelly).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Asteridae; euasterids I; Lamiales; Pedaliaceae;
OC Sesamum.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. 4294; TISSUE=COTYLEDON;
RA SHOUJI K.;
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: CHLOROPLAST OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY
CC ACIDS, IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT
CC TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.
CC -!- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).
CC -!- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/ OR BE INVOLVED IN METAL ION BINDING.
CC -!- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
CC -----
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core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
 [1]
 SEQUENCE FROM N.A.
 STRAIN=CV. 651-2-5-7-4;
 SINGH S.P., VAN DER HEIDE T., MCKINNEY S., GREEN A.;
 "Nucleotide sequence of a cDNA from Brassica juncea encoding a
 microsome omega-6 desaturase";
 (In) Plant Gene Register PGR95-107.
 FUNCTION: ER (MICROSOMAL) OMEGA-6 FATTY ACID DESATURASE INTRODUCES
 THE SECOND DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS.
 IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
 CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
 ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
 PHOSPHOLIPIDS (BY SIMILARITY).
 PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
 SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
 DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
 AND/OR BE INVOLVED IN METAL ION BINDING.
 SIMILARITY: TO OTHER PLANT ER OMEGA-6 FATTY ACID DESATURASES.
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 or send an email to license@isb-sib.ch).

 DR EMBL: X91139; CAA62578.1; -
 DR PFAM: PF00487; FA_desaturase; 2.
 Oxidoreductase; Fatty acid biosynthesis; Endoplasmic reticulum;
 KW Transmembrane
 FT TRANSMEM 56 76 POTENTIAL.
 FT TRANSMEM 84 104 POTENTIAL.
 FT TRANSMEM 117 137 POTENTIAL.
 FT TRANSMEM 180 200 POTENTIAL.
 FT TRANSMEM 226 246 POTENTIAL.
 FT TRANSMEM 253 273 POTENTIAL.
 FT DOMAIN 105 109 HISTIDINE BOX 1.
 FT DOMAIN 141 145 HISTIDINE BOX 2.
 FT DOMAIN 316 320 HISTIDINE BOX 3.
 FT SEQUENCE 384 AA; 44315 MW; 13BECED8 CRC32;

 Query Match 6.0%; Score 137.5; DB 1; Length 384;
 Best Local Similarity 21.1%; Pred. No. 0.00014;
 Matches 80; Conservative 54; Mismatches 135; Indels 111; Gaps 20;
 QY 56 DKLRMPKINPSF-----ELPPQAAVNEAQEDFRKLREELATGMDASPLWYSYKIS 108
 DB 19 DTLKRVPCETPTTVCGLKKAIPHCFCRSPRSFYLWDIVASCF-----YYVA 70
 QY 109 TTLGLVGLYFLMVQYQYFI-----GAVLLGMHYQOMGLSHDICHQTEKRNW 159
 DB 71 TT-----YFLLPPLSYVAMPLYWACQGVVLTGV-----WVIAHECGHAFSDYQW 117
 QY 160 -NNLVGLVFGNGL--QGFSVTCWKDRNNAHSAATNVQGHG-----PDID-----NL 202
 DB 118 LDDTVGLIFSHFLVLPYFS--WKYSHRRHSHNTGSLERDEVFPVKKSDIKWYKLYNN 174
 QY 203 P-----PLAWSDDVTRASPISKRLQFQYFLVICILLRFTWCQCVL 247
 DB 175 PLGRIVMLTVQTLGFWPLWAFNVSCRYPGE-----FACHF 211
 QY 248 TVRS--LKDRDNQVRSQ-YKKEAIGLALHWTALKALFLFFMPSILTSLLVFSVSLVGG 304
 DB 212 HENAPIYNDRE---RLQIYVSDAGILAVCY---GLYRYAAAGQVASYCLIGVPLLIYN 264
 QY 305 FGAIIVFVFNH--YP-LEKIGDPVWGHGFSVGQIHTMIRRGITDWFEGGLNVOIEHH 362
 DB 265 AFLVLITYLQHTPHSLPHYDSSEWD---WLRGAL-ATVDRDYGILNKVFNHTDTHVAHH 320

QY 363 LWPTLPRHNLTAYSYQVEQL 382
 DB 321 LFTMPHYHAMEVTKAIKPI 340
 RESULT 6
 ID_F62_SOYBN STANDARD; PRT; 383 AA.
 AC P48631;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE OMEGA-6 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM ISOZYME 2
 DE (EC 1.14.99.-).
 GN PAD2-2.
 OS Glycine max (Soybean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
 OC core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae;
 OC Glycine.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=EPICOTYL;
 RX MEDLINE; 96151506.
 RA HEPPARD E.P., KINNEY A.J., STECCA K.L., MIAO G.H.;
 RT "Developmental and growth temperature regulation of two different
 microsomal omega-6 desaturase genes in soybeans.";
 RL Plant Physiol. 110:311-319(1996).
 CC FUNCTION: ER (MICROSOMAL) OMEGA-6 FATTY ACID DESATURASE INTRODUCES
 THE SECOND DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS.
 IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
 CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
 ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
 PHOSPHOLIPIDS.
 PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
 SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
 DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
 AND/OR BE INVOLVED IN METAL ION BINDING.
 SIMILARITY: TO OTHER PLANT ER OMEGA-6 FATTY ACID DESATURASES.
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 or send an email to license@isb-sib.ch).

 DR EMBL: L43921; AAB00860.1; -
 DR PFAM: PF00487; FA_desaturase; 2.
 Oxidoreductase; Fatty acid biosynthesis; Endoplasmic reticulum;
 KW Transmembrane
 FT TRANSMEM 61 81 POTENTIAL.
 FT TRANSMEM 85 105 POTENTIAL.
 FT TRANSMEM 117 137 POTENTIAL.
 FT TRANSMEM 179 199 POTENTIAL.
 FT TRANSMEM 225 245 POTENTIAL.
 FT TRANSMEM 249 269 POTENTIAL.
 FT DOMAIN 105 109 HISTIDINE BOX 1.
 FT DOMAIN 141 145 HISTIDINE BOX 2.
 FT DOMAIN 315 319 HISTIDINE BOX 3.
 FT SEQUENCE 383 AA; 43967 MW; CAL65721 CRC32;

 Query Match 5.9%; Score 134.5; DB 1; Length 383;
 Best Local Similarity 21.8%; Pred. No. 0.00026;
 Matches 83; Conservative 56; Mismatches 144; Indels 97; Gaps 21;
 QY 56 DKLRMPKINPSFEL-----PQAAVNEAQEDFRKLREEL-----IATGMDASP 100
 DB 19 DPLKRVPEKQFSLSQIKKAIKPPHCFQSVLRSPVYVDLTIAFLCYVYVATHYFLLP 78
 QY 101 LWYSKISTTLGLVGLYFLMVQYQYFI GAVLLGMHYQOMGW-LSHDICHQTEKRNW 159

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FT TRANSIT 1 64 CHLOROPLAST (BY SIMILARITY).
FT CHAIN 65 443 OMEGA-6 FATTY ACID DESATURASE.
FT DOMAIN 166 170 HISTIDINE BOX 1.
FT DOMAIN 202 206 HISTIDINE BOX 2.
FT DOMAIN 362 366 HISTIDINE BOX 3.
SQ SEQUENCE 443 AA: 50755 MW: C814102A CRC32:

Query Match 6.4%; Score 145; DB 1; Length 443;
Best Local Similarity 20.5%; Pred. No. 3.9e-05;
Matches 75; Conservative 55; Mismatches 131; Indels 104; Gaps 17;

QY 71 PPOAAVNEAED-----FRKLREEL-----IATGMFDASP-----LWYSYKISTT 110
DB 71 PPSADNAEDREOLAESYGFQIGQDLPDNLTKDINDTLTPKEVFEDDVKAMKSVLSVIT 130
QY 111 LGLGVLYFLMVOYQMYFI-----GAVLLGMHYQOMGWSLSDHCHHOTFKRNNNNLV 163
DB 131 --SYALGLFMIKAPWYLLPLAWAWTGTAVTGFV-----IGHDCAKHSKKNKLVEDIV 183
QY 164 GLVFGNGLOGFSVTCWKDRHNAHSATNVQGHDPDIDNLPPLAWSEDDVTRASPISRKLI 223
DB 184 GTLAEPLV-YYPEPRFKRHRHAKTNMLVHDTANQVPP-----EEDF-----SSPVLKRAI 236
QY 224 QF-----QOYFVLY-----ICILLRIWCFQCY-----LTVRSKLRD 256
DB 237 IFGYPPIRWLSIAHVNWHNFNKRPRSEVNRVKISLACVAFAMVAGWPLII----- 290
QY 257 NOFYRSQYKEAIGLALHWTLLKALFLHFMPSILTSLLVFFVSELVGGFGIAIVFMNHY 316
DB 290 -----YKVGVLGVKFWLMPWLGYHFWMS-----TFTMVHHTAP-----HI 325
QY 317 PLEKIDPDVWDGHGFSVGOIHETMNRIRGIITDWFEGGLNQYIEHHLWPTLPRHNLTAVS 376
DB 326 PKPADE--WNA-----AAQLNGIVHCDYPSWIELCHDINVHPHISPIPSYNLRAAH 380
QY 377 YOVEQ 381
DB 381 QSIQE 385

RESULT 4
FD61-SOYBN STANDARD; PRT; 387 AA.
AC FD61-SOYBN
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE OMEGA-6 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM ISOZYME 1
GN FAD2-1.
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae;
OC Glycine.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SEED;
RX MEDLINE; 96151506.
RA HEPPARD E.P., KINNEY A.J., STECCA K.L., MIAO G.H.;
RT "Developmental and growth temperature regulation of two different
RT microsomal omega-6 desaturase genes in soybeans.";
RL Plant Physiol. 110:311-319(1996).
CC -!- FUNCTION: ER (MICROSOMAL) OMEGA-6 FATTY ACID DESATURASE INTRODUCES
CC THE SECOND DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS.
CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
CC PHOSPHOLIPIDS.
CC -!- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
CC -!- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN DEVELOPING SEEDS.

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CC -!- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/OR BE INVOLVED IN METAL ION BINDING.
CC -!- SIMILARITY: TO OTHER PLANT ER OMEGA-6 FATTY ACID DESATURASES.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: L43920; A800859.1;
DR PFAM: PF00487; FA_desaturase; 2.
KW Oxidoreductase; Fatty acid biosynthesis; Endoplasmic reticulum;
KW Transmembrane.
FT TRANSMEM 54 74 POTENTIAL.
FT TRANSMEM 87 107 POTENTIAL.
FT TRANSMEM 121 141 POTENTIAL.
FT TRANSMEM 183 203 POTENTIAL.
FT TRANSMEM 227 247 POTENTIAL.
FT TRANSMEM 251 271 POTENTIAL.
FT DOMAIN 109 113 HISTIDINE BOX 1.
FT DOMAIN 145 149 HISTIDINE BOX 2.
FT DOMAIN 319 323 HISTIDINE BOX 3.
SQ SEQUENCE 387 AA: 44662 MW: 9F81BE96 CRC32:

Query Match 6.1%; Score 140; DB 1; Length 387;
Best Local Similarity 21.3%; Pred. No. 8.9e-05;
Matches 83; Conservative 56; Mismatches 162; Indels 88; Gaps 19;

QY 58 LKRMKPINPSF-----ELPPOAAVNEAEDFRKLREELIATGMFDASPLWYSYKISTT 110
DB 26 LSRVPNTKPPFTVGQLKKAIPHCFCORSLTSESYV-----VYDLSFAFIY-IATT 76
QY 111 LGLGVLYFLMVOYQMYFI-----GAVLLGMHYQOMGWSLSDHCHHOTFKRNN--NVLGLVLF 167
DB 77 YFHLPPQPSLIAMIPIYVWLGCLTGV-----WVIAHECGHAFSKYQWDDVVGLTL 130
QY 168 NGNL--QGFSVTCWKDRHNAHSATNVQGHDPDIDNLPPLAWSEDDVTRASPISRKLIQF 225
DB 131 HSTLLVYPFS---WKISHRRHSNTG-----SLDRDEVFVFKPKS-KYAVF 172
QY 226 QOYI-----FLVICILLRIWCFQCVLTVRSKLRDNOFYRSQYKKEA----- 269
DB 173 SKYLNPLGRVSLVLTATIGWPMYLAFAV---SGRPYDSFASHYPIYAPISNRRRLLI 229
QY 269 --LGLALHWTLLKALFLHFMPSILTSLLVFFVSEL-VGGFGIAIVFMN-HYPLEKIGDP 324
DB 230 YVSDVALFSVTSYLYRVATLKGVLVLLCVYGVPLLVINGFLVITYLQHTHEALPHYDSS 289
QY 325 VWDGHGFSVGOIHETMNRIRGIITDWFEGGLNQYIEHHLWPTLPRHNLTAVSQVEQLC- 384
DB 290 EWD---WLKAL-ATWDRDYGLNKVFFHHTDTHVAHLEFSTMPHYHAMEATNAIKPILG 345
QY 384 ---QKHNLPYRNP-----PHEG 398
DB 346 EYQFDDTTPYKALWREARECLYVEPDEG 374

RESULT 5
FD6E-BRAJU STANDARD; PRT; 384 AA.
ID FD6E-BRAJU
AC Q39287;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE OMEGA-6 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (EC 1.14.99.-)
DE (DELTA-12 DESATURASE).
OS Brassica juncea (Leaf mustard) (Indian mustard).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;

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Result No.	Score	Query		ID	Description
		Match	Length		
1	239	10.5	359	LLDC_SVNY3	Q08971 synecchocyst
2	145.5	6.4	418	FD6C_ARATH	P46312 arabidopsys
3	145	6.4	443	FD6C_BRANA	P48627 brassica na
4	140	6.1	387	FD61_SOYBN	P48630 glycine max
5	137.5	6.0	384	FD6E_BRAJU	Q39287 brassica ju
6	134.5	5.9	383	FD62_SOYBN	P48631 glycine max
7	134	5.9	383	FD6E_ARATH	P46313 arabidopsys
8	127	5.6	447	FD3C_SSSIN	P48620 sesamum ind
9	126.5	5.5	380	FD3E_PPHAU	P32291 phaseolus a
10	123.5	5.4	342	CDTA_SVNY3	P54972 agrobacteti
11	120	5.3	351	DETS_SVNY3	P20388 synecchocyst
12	120	5.3	383	FD32_BRANA	P48624 brassica na
13	118	5.2	379	FD3E_TOBAC	P48626 nicotiana t
14	117	5.1	453	FD3C_SOYBN	P48621 glycine max
15	116.5	5.1	447	FD6C_SPIOI	P48629 spinacia ol
16	116.5	5.1	460	FD3C_SPCCO	P48619 ricinus com
17	114	5.0	380	FD3E_SOYBN	P48625 glycine max
18	113.5	5.0	424	FD6C_SOYBN	P48628 glycine max
19	111	4.9	431	CYBR_DROME	P19967 drosophila
20	110	4.8	351	DESA_SPIOI	Q54794 spirulina p
21	110	4.8	404	FD3C_BRANA	P48618 brassica na
22	109	4.8	591	CYB2_YEAST	P00175 saccharomyc
23	108.5	4.8	435	FD3D_ARATH	P48622 arabidopsys
24	107.5	4.7	446	FD3C_ARATH	P46310 arabidopsys
25	106.5	4.7	573	CYB2_HANAN	P09437 hansenula a
26	105	4.6	386	FD3E_ARATH	P48623 arabidopsys
27	98	4.3	120	CYB5_YEAST	P40312 saccharomyc
28	97	4.2	359	ACOD_HUMAN	O00767 homo sapien
29	95.5	4.2	358	ACOD_RAT	P07308 rattus norv
30	95	4.2	355	ACOI_MOUSE	P13516 mus musculus
31	95	4.2	133	CYB5_BOVIN	P00171 bos taurus
32	95	4.2	133	CYB5_HUMAN	P00167 homo sapien
33	93.5	4.1	134	CYB5_MUSDO	P49096 musca domes
34	93	4.1	371	FD31_BRANA	P46311 brassica na
35	92.5	4.1	583	CYB_SULAC	P39480 sulfolobus
36	92	4.0	334	ACOD_MSAU	Q64420 mesocricetu
37	91.5	4.0	859	NIA_PICAN	P49050 pichia angu
38	91.5	4.0	524	YE33_SVNY3	P74217 synecchocyst
39	91	4.0	893	NIA_LEPMC	P36842 leptosphaer

Matches 83; Conservative 56; Mismatches 162; Indels 88; Gaps 19;

Qy 58 LKRPKINPSF-----ELPQAAVNEAQEDFKRLREELIATGMDASPLWYKISTT 110
 Db 26 LSRVNTKPPFTVGOLKKAIPHCQFSLTSFSYV-----YIDLSEAFIFY-IATT 76
 Qy 111 LGLGVLYGFLVVOYQYFI--GAVLLGHYQMGWLSHDICHQTFKKNRW--NNLVGLVF 167
 Db 77 YFHLPPQFSLIAWPIYVWLOCLTGV-----WVAHECGHAFSKYQWDDVVGTL 130
 Qy 168 GNLG--QGFSVTCWKDRNNAHNSATNVQGHDDIDNLPPLAWSEDDVTRASPIRKLQF 225
 Db 131 HSTLLVPYFS--WKSHRRHSNTG-----SLDRDEVFPKPKS-KVAFW 172
 Qy 226 QOQY-----FLVICILLRFWCFOCVLTVRSLKDRDQFYRSQYKKEA----- 269
 Db 173 SKYLNPLGRAVSLTITIGWPMYLAENV---SGRPVDSFASHYHPYAPYSNRERLLI 229
 Qy 269 --IGLALHWTALKALFHFEMPSILTSLLVFFVSEL-VGGFGIAIVFVFN--HYPLEKIGDP 324
 Db 230 YVSDVALFSVTSYLRVATLAKGLWLLCVGYVPLLVNGFLVTITLYLQHTHEALPHYDSS 289
 Qy 325 VMDGHGFSVGQIHETMNTTRGIITDFFGGLNYQIEHLMPTLPHRNLTAVSQVEQLC- 384
 Db 290 EWD---WLKGAAL-ATMDRDYGLNKVFFHITDTHVAHHLFSTMPHYHAMEATNAIKPILG 345
 Qy 384 --QKHNLPIYRNPL-----PHEG 398
 Db 346 EYQFDPTPFYKALWREARECLYVEPDEG 374

RESULT 14

T14269
 delta-12 oleate desaturase - common sunflower
 C:Species: Helianthus annuus (common sunflower)
 C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
 C:Accession: T14269
 R:Hongtrakul, V.; Slabaugh, M.B.; Knapp, S.J.
 submitted to the EMBL Data Library, February 1997
 A:Description: Sunflower delta-12 oleate desaturase.
 A:Reference number: Z17949
 A:Accession: T14269
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-378 <HON>
 A:Cross-references: EMBL:U91341; NID:g2290403; PID:g2290404
 A:Experimental source: strain Mammoth
 C:Function:
 A:Description: desaturates oleic acid to linoleic acid

Query Match 6.18; Score 139; DB 2; Length 378;

Best Local Similarity 21.4%; Pred. No. 7.8e-05;
 Matches 76; Conservative 52; Mismatches 139; Indels 88; Gaps 19;

Qy 58 LKRPKINPSF-----ELPQAAVNEAQEDFKRLREELIATGMDASPLWYKISTT 110
 Db 16 LDRVPHAKPFTIGDLKKAIPHCQFSLTSFSYVLSDLTITAVL-----YHIATT 67
 Qy 111 LGLGVLYG-----LMVOYQYFI--GAVLLGHYQMGWLSHDICHQTFKKNRW-N 160
 Db 68 -----YFHHPLPPLSSIAWASVWVVGCVLTGV-----WVAHECGHAFSDYQWVD 114
 Qy 161 NLVGLVFGNLG--QGFSVTCWKDRNNAHNSATNVQGHDDIDNLPPLAWSEDDVTRASPI 218
 Db 115 DTVGFLHSLLLVPYFS--WKYSHRRHSNTG-----SLRDEV--FVPK 155
 Qy 219 SRKLQFQOQYF-----LVICILLRFWCFOCVLTVRSLK-DR-----DNQF 259
 Db 156 SRSKVPWYSKYNNTVGRIVSMFVTLTGWPLYLAFNVGRPYDRFACHYVPTSPMYNER 215
 Qy 260 YRSQYKKEAIGLALHWTALKALHFLFFMPSILTSLLVFFVSELVGGFGIAIVFNMH-YPL 318

Db 216 KRYQIVMSDIGIVI--TSFILRYVMAKGLVWVICVGYVPLMVVNAFLVLTLYLOHTHP- 273
 Qy 319 EKIGDPVWDGHGS--VQGIHETMNTTRGIITDFFGGLNYQIEHLMPTLPRHN 371
 Db 273 ---GLPHYDSSSEWEWLKALG-ATVDRDYGVLENKVFHFHITDTHVVVHHLFSTMPHYN 323
 RESULT 15
 T11959
 fatty-acid desaturase - red alga (Cyanidium caldarium) chloroplast
 C:Species: Chloroplast Cyanidium caldarium
 C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
 C:Accession: T11959
 R:Gloeckner, G.; Rosenthal, A.; Valentin, K.
 submitted to the EMBL Data Library, September 1997
 A:Description: Organisation of 46 kb of the Cyanidium caldarium Rk1 plastid genom
 A:Reference number: Z17374
 A:Accession: T11959
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-287 <GLO>
 A:Cross-references: EMBL:AF022186; NID:g2465730; PID:g2465769
 A:Experimental source: strain Rk1
 C:Genetics:
 A:Gene: desa
 A:Genome: chloroplast
 C:Keywords: chloroplast

Query Match 6.08; Score 136.5; DB 2; Length 287;
 Best Local Similarity 23.08; Pred. No. 9.2e-05;
 Matches 61; Conservative 34; Mismatches 103; Indels 67; Gaps 14;

Qy 113 LGVLGYFLVVOYQYFI--GAVLLGHYQMGWLSHDICHQTFKKNRWNNLVGLVFGNLQ 172
 Db 35 ISIFSYPILHLNSSICFLINLLSLH--LGTVIDSSHKAADNKYINFYFIGHISAFEL- 92
 Qy 173 GFSVTCWKDRNNAHNSATNVQGHDDIDNLPPLAWSEDDVTRASP---ISRKLQFQOY 229
 Db 92 GFSPFVFSRVHMQHAYVNDANNDPD-----HEVSTAGPLMLIASRFFYHEVYF 140
 Qy 230 FLVICILLRFWCFOCVLTVRSLKDRDQFYRSQYKKEAIGLALHWTALKALHFLFFMPSI 289
 Db 141 F-----QRKLW-----RNKLEIWI--WARTLLICLLFI-AF 169
 Qy 290 LTSLLVF-----FVSELVGGFGIAIVV-FMNHYPLEKIGDPVWDGHGFSVGQIHETMNR 343
 Db 170 ETNILEYVFKWFCPALVVGFGALGCLCFDYLPHYFF-KYTDR-WHN-----SCVYPSKFLN 222
 Qy 344 RGIITDFFGGLNYQIEHLMPTLP 368
 Db 223 LAIF-----GQNYHLVHHLWPSAP 241

Search completed: February 24, 2000, 22:01:39
 Job time: 17316 sec

QY 204 PLAWSEDDVTRASPISRLKIQOQYFVLVICILLRIFWCFVCLTVRSKDRDNOFYRSQ 263
 Db 132 -----HFVSTGGPL-----FLIAARFFVHEIFFKRLRL-----RK 162
 QY 264 YKKEAIGLALHWTIKAL-----PHLFMPSTLSLLVFFVSELVGGFGIAIVFMN 314
 Db 163 YE-----LLEFSLRSLVLFVIFLGHYIGFVFMN---YWFVPALI--VGIALGLEFD 211
 QY 315 HYLEKIGDPVWDGHSVGOIHETMNRIRGIITDWFEGGLNVOIEHHLWPTLP 368
 Db 212 YLPHR-----PFQERNRKNARVYSP-----ILNLIFGQNYHLIHLWPSIP 255
 RESULT 11
 T08136
 probable omega-6 desaturase (EC 1.14.99.-) precursor, chloroplast - rape
 C:Species: Brassica napus (rape)
 C:Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 21-May-1999
 C:Accession: T08136
 R:Hit: W.D.; Carlson, T.J.; Booth, J.R.; Kinney, A.J.; Stecca, K.L.; Yadav, N.S.
 Plant Physiol. 105, 635-641, 1994
 A:Title: Cloning of a higher-plant plastid omega-6 fatty acid desaturase cDNA and its ex
 A:Reference number: 216109; MUID:94345008
 A:Accession: T08136
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-443 <HIT>
 A:Cross-references: EMBL:L29214; NID:9457630; PID:9457631
 A:Experimental source: seed
 C:Genetics:
 A:Genome: nuclear
 C:Superfamily: omega-3 fatty acid desaturase
 C:Keywords: chloroplast; fatty acid metabolism; oxidoreductase
 Query Match 6.4%; Score 145; DB 2; Length 443;
 Best Local Similarity 20.5%; Pred. No. 2.8e-05;
 Matches 75; Conservative 55; Mismatches 131; Indels 104; Gaps 17;
 QY 71 PPOAAVNEAQED-----FRKLREL-----IATGMFDASP-----LMYSYKISTT 110
 Db 71 PPSADNAEDRQLAESYGFQIGQDLPDNLKIDMDLPKREVFIDVDKAWKSVLISVT 130
 QY 111 LGLGVGLVLMVQYQYFI-----GAVLLGMHYQOMGWSHDICHQHTKRNWNMLV 163
 Db 131 --SYALGLFMIAKAPWYLLPLAWMTGTAVTGFFV-----IGHDCAKHSFSKNKLVEDIV 183
 QY 164 GLVFGNGLOGFSVTCWCKDRHNAHSATNVQGHDPDIDNLPLAWSEDDVTRASPISRLKI 223
 Db 184 GTLAFPLV--YPYEPWRKDRHNAHSATNVQGHDPDIDNLPLAWSEDDVTRASPISRLKI 236
 QY 224 QF-----QQYFLV-----ICILLRFWCFV-----LTVRSKDRD 256
 Db 237 IFGVPTRPWLISIAHWVHNLKRFSEVNRVKISLACVAFNAVGVPLII-----290
 QY 257 NQFYRSQYKKEAIGLALHWTIKALPHLFMPSTLSLLVFFVSELVGGFGIAIVFMNHY 316
 Db 290 -----YKVGVLGVKFWLMPWLGHEFMS--FTNVVHTAP-----HI 325
 QY 317 PLEKIGDPVWDGHSVGOIHETMNRIRGIITDWFEGGLNVOIEHHLWPTLP 376
 Db 326 PFKPADE--WNA---AQQLNGTVHCYPSWIEILCHDINVIHPIHSPRIPSYNLAH 380
 QY 377 YQVEQ 381
 Db 381 QSIQE 385

RESULT 12
 S75038
 hypothetical protein sl11611 - Synchocystis sp. (strain PCC 6803)
 C:Species: Synchocystis sp.
 A:Variety: PCC 6803

C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 21-Aug-1998
 C:Accession: S75038
 R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyaji
 O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.;
 DNA Res. 3, 109-136, 1996
 A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synech.
 S.
 A:Reference number: S74322; MUID:97061201
 A:Accession: S75038
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-369 <KAN>
 A:Cross-references: EMBL:D90910; GB:AB001339; NID:91652956; PID:d1018633; PID:g16
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
 C:Genetics:
 A:Start codon: GTG

Query Match 6.3%; Score 143.5; DB 2; Length 369;
 Best Local Similarity 23.4%; Pred. No. 3e-05;
 Matches 83; Conservative 51; Mismatches 126; Indels 95; Gaps 19;
 QY 79 AQEDFRKLRELIAATGMFDASPLWYSYKISTTGLGVGLGYFLM-----VOYQM 126
 Db 4 AQSEYVKKLRPLLPPEAFQADP-----KKLVILGLN-LGIYVAGLTIAHRLHQPQWLW 57
 QY 127 YFIG-AVLLGMHYQOMGWSHDICHQHTKRNWNMLVGLVFGNGLOGFSVTCWKDRUN- 185
 Db 58 LFLPMALLMGNSVTVFLFGSHDLMHGVSVKRSKISYLSLLGLSLMWPSPQMSRLHNO 117
 QY 185 AHSATNVQGHDPDIDNL--PPLAWSEDDVTRASPISRLKIQOQYFVLVICILLRFTWC 242
 Db 118 VHNNTN-SLRDPDRNVLHEQPKTWGKIHLFAPSGE-----VNTLWL 160
 QY 243 -----FOCVLTVR-----SLKDRDNOFYRSQYKKEAIGLALHWT 276
 Db 161 IFMGWTANGVINFRNLISVLEFTGNGNADFVPAFTVKAQDRQ--RIMLELAIG-AVH-- 216
 QY 277 LKALFHLFF--MPSILTSLLVFFVSELVGGFGIAIVFMNHY--PLEKIGDPVWDGHSFS 332
 Db 216 LSILFLQFQILPIILGYFLFIFLGHAMGF-----YVTNHLACPMTDINDP----- 264
 QY 333 VQGHETMNRIRGIITDWFEGGLNVOIEHHLWPTLPRLNLTAVSYQ-VEQLCOKH 386
 Db 264 ---LVNSYSLRMPKLFDCLFHFNFYHTEHLEFP-----DVNSDYPLVQDQLQTH 310

RESULT 13
 T07687
 omega-6 desaturase FAD2-1, microsomal - soybean
 C:Species: Glycine max (soybean)
 C:Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 26-Aug-1999
 C:Accession: T07687
 R:Heppard, E.P.; Kinney, A.J.; Stecca, K.L.; Miao, G.H.
 Plant Physiol. 110, 311-319, 1996
 A:Title: Developmental and growth temperature regulation of two different microsc
 A:Reference number: 216095
 A:Accession: T07687
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-387 <HEP>
 A:Cross-references: EMBL:L43920; NID:9904151; PID:9904152
 A:Experimental source: seed
 C:Genetics:
 A:Gene: FAD2-1
 C:Function:
 A:Description: involved in production of polyunsaturated lipids; plays a major rc
 A:Note: strongly expressed in developing seeds
 C:Superfamily: Omega-3 fatty acid desaturase

Query Match 6.1%; Score 140; DB 2; Length 397;
 Best Local Similarity 21.3%; Pred. No. 6.5e-05;

QY 315 HYP-----LEKIGDPVWDGHSVGOIHETNMIRRIITDWFEGGLNLYQIEHHLWPT 366
 Db 257 HFPDGAKEFKYTDIGEP--KGWY-LRQMLGSANFNAGPALRFMSGNLCHQIEHHLYPD 313
 QY 367 LPRHNLTAVSQVQLCKQKHNLPY 390
 Db 314 LPSNRLHEISVRREVCDYDLPY 337

RESULT 8
 T10789
 omega-6 desaturase, microsomal - upland cotton
 C:Species: Gossypium hirsutum (upland cotton)
 C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 26-Aug-1999
 C:Accession: T10789
 R:Li, Q.; Singh, S.P.; Green, A.; Sharp, P.J.; Marshall, D.R.
 submitted to the EMBL Data Library, March 1999
 A:Description: Isolation and characterisation of two different microsomal omega-6 desaturase
 A:Reference number: 217145
 A:Accession: T10789
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-383 <LIU>
 A:Cross-references: EMBL:Y10112; NID:el393524; PID:e321496
 A:Experimental source: subspecies Deltapine-16
 C:Function:
 A:Description: Involved in production of polyunsaturated lipids
 C:Superfamily: omega-3 fatty acid desaturase

Query Match 6.5%; Score 149; DB 2; Length 383;
 Best Local Similarity 22.8%; Pred. No. 1e-05;
 Matches 82; Conservative 49; Mismatches 156; Indels 76; Gaps 19;

QY 55 FDKLRMPKINPSFEL-----PPQAAVNEAQEDFRKREELIATGMFDASPLWYSYKI 107
 Db 18 FNSLKRVPYSKPPFTLSEIKKAIPPHCFQSVLRFSYLLYDFILASLF-----YHV 69
 QY 108 STTLGLGLVGLYFLMVQYQYFI--GAVLLGHVYQMGWLSHDICHQHTFKNRW--NNLVG 164
 Db 70 ATNYFNLPOALSNVAPLWAMQGCILTV-----WVIAHECGHAFSDYQWLDPTVG 123
 QY 165 LVFENGIL--QGFSVTCWKDRHNAHSATNVQGHDPDIDNLP-----LAWSEDDVTRASPI 218
 Db 124 LILHSSLLVPYFS--WKYSRRRHNTQSLERDEVE--VPKKSGLRWAKHFN--NPP 176
 QY 219 SRKLIQFOQYFLVICILLRFICFCQCVLTVRS-----LKDNDN-QFYR 261
 Db 177 GR-----FLSITITLQTLGWPLYLAFNVAGRPYDRFACHYDPYGPFIQFSDRELQIYI 227
 QY 262 SQYKKEAIGLALHTLALFHLFMPISILTSLLVFFVSELSVGGFIAIVFMNH--YP-LE 319
 Db 228 S-----DAGVLAVAY----ALRLVLAKGVWVISYGVPLLVNFAFLVMTYLOHTHPSLP 280
 QY 320 KIGDPVWDGHSVGOIHETNMIRRIITDWFEGGLNLYQIEHHLWPTLPRHNLTAVSQV 379
 Db 281 HYDSSMD---WMRGAL-STVDRDYGLNLKVFHNITDTHVAHLFSTMPHYHAWATKAI 336
 QY 380 EQL 382
 Db 337 KPI 339

RESULT 9
 T15043
 fungal elicitor-induced protein - parsley
 C:Species: Petroselinum crispum (parsley)
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
 C:Accession: T15043
 R:Kirsch, C.; Hahlbrock, K.; Somssich, I.E.
 Plant Physiol. 115, 283-289, 1997
 A:Title: Rapid and transient induction of a parsley microsomal delta 12 fatty acid desaturase
 A:Reference number: 218274; MUID:97451781

A:Accession: T15043
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-383 <KIR>
 A:Cross-references: EMBL:U86374; NID:g2501791; PID:g2501792
 C:Genetics:
 A:Gene: ELI12

Query Match 6.5%; Score 147.5; DB 2; Length 383;
 Best Local Similarity 23.1%; Pred. No. 1.4e-05;
 Matches 81; Conservative 45; Mismatches 154; Indels 71; Gaps 16;

QY 54 AFDKLRMPKINPSF-----ELPQAAVNEAQEDFRKREEL-ITGMFDASPLWYSY 105
 Db 17 AAELKRAPEHEKPPFTIGDLKKAIPAHCFQKSLVTSFYLIQDLFMAYLFVATNYDQ 76
 QY 106 KISTTLGLGLVGLYFLMVQYQYFI--GAVLLGHVYQMGWLSHDICHQHTFKNRW--NNLVG 164
 Db 77 YLTPFNYVAAVIAVQ-----GCVLTG-----AWVVGHECHDAFSNYNNINDLVG 124
 QY 165 LVFENGIL--QGFSVTCWKDRHNAHSAT-----NVQGHDPDIDNLP----- 205
 Db 125 LVVHSSLLVPYFS--WKYSRRRHANTQSLERDEVEVVPKSNIRNYKLLNN-PPGRV 180
 QY 205 LAWSEDDVTRASPISRKLIQFOQYFLVICILLRFICFCQCVLTVRSKDRDNQFYRSQY 264
 Db 181 LVN-----LTTLLIGFLYLMFNVSCHKYER-----TSHYDPSPLYSORE 222
 QY 265 KKEAI--GLALHTLALFHLFMPISILTSLLVFFVSELSV--GGFGTAIVVFMNHYLEK 320
 Db 223 RKEIIVSDIALLAVIYDLYOLVLAKGFAWVFCVYGGPLLVNGWFLVLTILNTHPSLPY 282
 QY 321 IGPVWDGHSVGOIHETNMIRRIITDWFEGGLNLYQIEHHLWPTLPRHN 371
 Db 283 YDSTEND--WLRGALC-TVDRDYGLNLKVFHNVCNAHVCHHIFSMPIPHY 329
 RESULT 10
 S77365
 hypothetical protein s111468 - Synechocystis sp. (strain PCC 6803)
 C:Species: Synechocystis sp.
 A:Variety: PCC 6803
 C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 21-Aug-1998
 C:Accession: S77365
 R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Miyajin, O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.;
 DNA Res. 3, 109-136, 1996
 A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
 A:Reference number: S74322; MUID:97061201
 A:Accession: S77365
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-312 <KAN>
 A:Cross-references: EMBL:D90906; GB:AB001339; NID:g1652492; PID:d1018201; PID:g1616
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
 C:Genetics:
 A:Start codon: GTG

Query Match 6.4%; Score 147; DB 2; Length 312;
 Best Local Similarity 20.7%; Pred. No. 1.2e-05;
 Matches 61; Conservative 48; Mismatches 111; Indels 74; Gaps 13;

QY 87 REELIATGMFDASPLWYSYKISTTLGLGLVGLYFLMVQYQYFI--GAVLLGHVYQMGWLSH 146
 Db 24 KEFLQADGGENPVAMFGTAILMLA--NVFGWQWGLPHWLFCFSCSVLALHLS--GTVII 80
 QY 147 DICHHQTFKNRWNNLVGLVFGNG---LQGFSVTCWKDRHNAHSATNVQGHDPDIDNLP 203
 Db 81 DASHNAHR---NTIINAVLGHGSLMGALGFAPFTRVHLOHANNVNDPDPD----- 132

[illegible]

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 24, 2000, 22:01:38 ; Search time 19.68 Seconds
(without alignments)
1011.456 Million cell updates/sec

Title: PCT-US99-28555-4
 Perfect score: 2283
 Sequence: 1 MKSKRQALSPQLMEQTYDV.....LRYLAVFARMAEQPAGKAL 422

Scoring table: BLOSUM62

Searched: 142080 seqs, 47169319 residues

Database : PIR 62:★

Word size : 0

Number of hits that pass the threshold : 142080

```

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	498.5	21.8	458	2	S69358	hypothetical prote
2	428.5	18.8	444	2	JG0180	delta-6 fatty acid
3	420	18.4	444	2	T13155	delta-6 fatty acid
4	311.5	13.6	311	2	T08765	probable delta-6 f
5	239	10.5	359	2	S35157	Delta(6)-desaturas
6	216	9.5	368	2	S54809	linoleoyl-CoA desa
7	166.5	7.3	427	2	G70590	probable desat3 pro
8	149	6.5	383	2	T10789	omega-6 desaturase
9	147.5	6.5	383	2	T15043	fungal elicitor-in
10	147	6.4	312	2	S77365	hypothetical prote
11	145	6.4	443	2	T08136	probable omega-6 d
12	143.5	6.3	369	2	S75038	hypothetical prote
13	140	6.1	387	2	T07687	omega-6 desaturase
14	139	6.1	378	2	T14269	delta-12 oleate de
15	136.5	6.0	287	2	T11959	fatty-acid desatur
16	134.5	5.9	383	2	T07688	omega-6 desaturase
17	133.5	5.8	347	2	S43771	phosphatidylcholin
18	133	5.8	385	2	T09880	omega-6 desaturase
19	132	5.8	350	2	S43772	phosphatidylcholin
20	128	5.6	352	2	B69901	fatty-acid desatur
21	128	5.6	438	2	T15039	omega-3 fatty acid
22	127	5.6	349	2	S43770	phosphatidylcholin
23	126.5	5.5	380	2	T10898	probable omega-3 f
24	126.5	5.5	387	2	T09839	oleate 12-hydroxyl
25	125.5	5.5	431	2	T07685	omega-3 fatty acid
26	124	5.4	141	2	T15210	hypothetical prote
27	120	5.3	383	2	A44227	omega-3 fatty acid
28	120	5.3	351	2	T15159	phosphatidylcholin
29	120	5.3	383	2	T10480	Delta12 oleate des
30	120	5.3	382	2	T15042	omega-6 fatty acid
31	118	5.2	379	2	JC2555	omega-3 fatty acid
32	117	5.1	453	2	JQ2339	omega-3 fatty acid
33	117	5.1	447	2	S53309	n-6 fatty acid des
34	116.5	5.1	460	2	T10063	omega-3 fatty acid
35	114	5.0	380	2	JQ2338	omega-3 fatty acid

RESULT
JG0180
2

36	114	5.0	441	2	T030299
37	113.5	5.0	381	2	T039233
38	113.5	5.0	424	2	T07742
39	111	4.9	414	1	S05441
40	110	4.8	404	1	Q08112
41	110	4.8	383	2	T062338
42	110	4.8	351	2	S54359
43	109	4.8	591	1	CBBX2
44	108.5	4.8	333	2	T070039
45	107.5	4.7	446	2	T023336

ALIGNMENTS

1. **DESCRIPTION**

RESOLUT I
568358

508358 hypothetical protein - common sunflower
C:Species: Helianthus annuus (common sunflower)

C: Species: HERITAGE
C: Date: 15-Feb-1997

C:Accession: S68358

R; Sperling, P.; Schmidt, H.; Heinz,

Eur. J. Biochem. 232, 798-805, 1995

A;Title: A cytochrome-b(5)-containing fus

A; Reference number:

A;Accession: S68358

A; Status: preliminary

A;Molecule type: mRNA

A; Residues: 1-458 <SPE>

A;Cross-references: EMBL:X87143; NID:g1040

C;Superfamily: cytochrome b5 core homology

Query Match	21.8%;	Score 498.5;	DB 2;	Length 458;
Best Local Similarity	29.7%;	Pred. No. 7.1e-37;		
Matches 126;	Conservative	76;	Mismatches 181;	Indels 41

```

11 LQLMEOITYDVSAWNPHPGGAIEIENYQGRDATDAFVMVHFOEADKDKRMKPKNINPSPEL 70
   : : : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 35 ISILGVYNVTWEAKBEPGGDAPLINLAGQDDYDAFIAPHGTAW---KHLDKLETGYHL 91

Qy 71 PPOAAVNEAQEDFKRLREELIATGMFDASPLWSYK--ISTTLGLUGLVGYELMAYOYMY 127
   : : : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 92 -KDYOVSIDSRYRKLASFAGMEKKGHVGVIYSLCFVSLLSACVIVGVLYSGSFWIH 150

Qy 128 FIGAVILLGHYQOMGLSHSDICHHTFKNRNNMNVLGVFGNGLAGFSYTCWKDRHNHH 187
   : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db 151 MLSGAILGLAWMOIAYLGHDAGHYQMMAIRGNKKPAGIFIGNCITGISIAWWKWTNNAHH 210

Qy 188 SATNVGHDPDIDNPPLAMSE---DDVTTRA-----SPISRKLIOPQQ-YELVLCTI 235
   : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 211 IACNSLDYPDQLHPLMLAVSSKLFNSITSVFYGRQLTFDPLARFVSYQHLYLYPYIMCV 270

Qy 236 --LLRIWFQCQCVLTVRSLKRDNQFYRSQYKEAIGLAHWLTKALF--HLFFWPSTLT 291
   : : : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 271 ARVNLYLOTILLISKRPIDRG-----LNITGLTIFWTPPLLVSRLPNMPERVA 321

Qy 292 SLLVFVSELVGGFGIAIVVF-MNHYPLE-KIGDPWMDCHGFSVQGIHETNMIRRGITTD 349
   : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 322 FVLVSFCVT----GIGHOTFLNHFGSDVYVGPp--KGDWNFEQRGTGCTIDIACSSWMD 374

Qy 350 WFFGGLUNYQIEHHLWPTLPRLHNLTVAVSQVEOLCOQHNLIPYRNPLPHEGLVILLRYLAVF 409
   : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 375 WFFGGOLOLEHHLPRLPRLCHLRISIPICRECKKCNLPYVLSFYDANVTTLKTLRTA 434

```

RESULT
JG0180
2

Db 61 FWOCCGWLADHFLHHQVQDRFWGDLFGAFLGGVCQGFSSSWWKKHNTTHAARNVHGED 120
 QY 197 PDIDNPLPLAWSEDDVTRASPI-----SRKLIQFOQYFVLVICILLRFINCFQCVL 247
 Db 121 PDIDTHPLTWSEHALEMESDVPDEELTRWMSRFLVNTQWTFYFPLSFARLSWCLQSIL 180
 QY 248 TVRSLKDRDNOFYRSQYKK-----EAIGLALHWTALKALFLHFFMPSILTSLLVFFVSEL 301
 Db 181 FVLP-----NGQAHKPSGARVPISLVEQLSLAMHWTWYLATMFLFIKDPVNNLVFLVSOA 236
 QY 302 VGGFGIAIVFMNHYPLEKIGDPVWDGHGFSVGOIHETMNRRIITDWFEGGLNYQIEH 361
 Db 237 VCGNLLAIVFSLNHNHNGMPVISKEAVDMDFTKIITGRDVHPGLFANWFTGGLNYQIEH 296
 QY 362 HLWPTLPRHNLTAVSQVEQLCQKHNLPIYRNPLPHEGLVILLRYLAVFARMAEKOPA--- 419
 Db 297 HLFPSMPRHNFESKIOPAVETLCKYNYRYHTTGMEGTA-----EVSRLNEVSKAASK 350
 QY 419 -GKA 421
 Db 351 MGKA 354

RESULT 15

US-08-956-985-7
 ; Sequence 7, Application US/08956985
 ; GENERAL INFORMATION:
 ; APPLICANT: KNUTZON, DEBORAH
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
 ; TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
 ; NUMBER OF SEQUENCES: 28
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
 ; STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039
 ; CITY: PALO ALTO
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94306
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/956,985
 ; FILING DATE: 24-OCT-1997
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/834,033
 ; FILING DATE: 11-APR-1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/833,610
 ; FILING DATE: 11-APR-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: RAE-VENTER, BARBARA
 ; REGISTRATION NUMBER: 32,750
 ; REFERENCE/DOCKET NUMBER: CGNE.128.01US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (650) 328-4400
 ; TELEFAX: (650) 328-4477
 ; TELEX: N/A
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 355 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: not relevant
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-956-985-7

Query Match 24.7%; Score 565; DB 13; Length 355;
 Best Local Similarity 34.9%; Pred. NO. 9e-52;

Matches 127; Conservative 58; Mismatches 145; Indels 34; Gaps 6;
 QY 82 DFRKRLRELIATGDFDASPLWYSYKISTTTLGLGVLGFLMVOYOM-----YFIGNVLGM 136
 Db 1 EVRKLRTLFQSLGYDSSKAYAFKVSFNLCINGLSTVIVAKWGOTSTLANVLSAALLGL 60
 QY 137 HYQOMGHLSDICHHOFTKRNWNNLVGLVFGNGLOGFSVTCWKDRHNAHSATNVQCHD 196
 Db 61 FWOCCGWLADHFLHHQVQDRFWGDLFGAFLGGVCQGFSSSWWKKHNTTHAARNVHGED 120
 QY 197 PDIDNPLPLAWSEDDVTRASPI-----SRKLIQFOQYFVLVICILLRFINCFQCVL 247
 Db 121 PDIDTHPLTWSEHALEMESDVPDEELTRWMSRFLVNTQWTFYFPLSFARLSWCLQSIL 180
 QY 248 TVRSLKDRDNOFYRSQYKK-----EAIGLALHWTALKALFLHFFMPSILTSLLVFFVSEL 301
 Db 181 FVLP-----NGQAHKPSGARVPISLVEQLSLAMHWTWYLATMFLFIKDPVNNLVFLVSOA 236
 QY 302 VGGFGIAIVFMNHYPLEKIGDPVWDGHGFSVGOIHETMNRRIITDWFEGGLNYQIEH 361
 Db 237 VCGNLLAIVFSLNHNHNGMPVISKEAVDMDFTKIITGRDVHPGLFANWFTGGLNYQIEH 296
 QY 362 HLWPTLPRHNLTAVSQVEQLCQKHNLPIYRNPLPHEGLVILLRYLAVFARMAEKOPA--- 419
 Db 297 HLFPSMPRHNFESKIOPAVETLCKYNYRYHTTGMEGTA-----EVSRLNEVSKAASK 350
 QY 419 -GKA 421
 Db 351 MGKA 354

Search completed: February 25, 2000, 04:47:16
 Job time: 15462 sec

Db 368 FFTQIITGRDVHPLFANWETGGLNYQIEHHLFSPMRHNSKIQPAVETLCKKNVRY 427
QY 391 RNPDPHEGLVILLRLYLAFAKQPA-----GKA 421
Db 428 HTTGMEGTA-----EVSRLNEVSKAASKMGKA 456

RESULT 13
US-09-377-475-4
; Sequence 4, Application US/09377475
; GENERAL INFORMATION:
; APPLICANT: KNUZON, DEBORAH
; APPLICANT: MUKERJI, PRADIP
; APPLICANT: HUANG, YUNG-SHENG
; APPLICANT: THURMOND, JENNIFER
; APPLICANT: CHAUDHARY, SUNITA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
; OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LIMBACH & LIMBACH L.L.P.
; STREET: 2001 FERRY BUILDING
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/377.475
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: WARD, MICHAEL R.
; REGISTRATION NUMBER: 38,651
; REFERENCE/DOCKET NUMBER: CGAB 102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)433-4150
; TELEFAX: (415)433-8716
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 457 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-377-475-4

Query Match 27.2%; Score 622; DB 17; Length 457;
Best Local Similarity 32.7%; Pred. No. 1e-57;
Matches 149; Conservative 76; Mismatches 174; Indels 56; Gaps 11;

QY 2 KSKQALSPQLM--EQYDYSANWVHFGAGIEIYQGRDATDAFVMHFQEAFLK 59
Db 23 EGKDAEAPFLMIIDNKVDYDFVDPHGGG-VILTHVGKDGTDVDFHPEAAWETL- 81
QY 60 RMPKINSPFELPPQAAVNEAQEDF-----RKRLRELIATGMFDASPLWYSKISTT 110
Db 81 -----AFYVY---GDIDESDRTKNDPFAAEVRKRLTFLFSLGYDSSKAYAFKVSFN 131
QY 111 LGLGLVGLFYMVOYQM-----YFAGVLLGMHYQOMGLSHDICHQPFKRNWNNVGL 165
Db 132 LCINGLSTVIVAKWGQSTLANVLISALLGLFWQCQGLHADFHLHQVFQDRFGDLFGA 191
QY 166 VFGNGLOGFSVTCWKDRHNAHSATNVQGHDPDIDNLPPLAWSDDVTRASPI----- 219
Db 192 FLGGVCQCGFSSSMKKDKHNTHAAPNVHVEDPDIDTHTPLLTWSEHALEMFSVDPDELTR 251

QY 219 --SRKLIQOQQYFLVICILLRFTWCQCVLTVRSUKDRDNQOFYRSQYK-----EAIG 270
Db 252 MWSRFMVLNQWTFYFPLSFARLSWCLQSILFVLP-----NGQAHKPSGARVPISLVEQLS 307
QY 271 LALHTLTKALFHLFEMPSILTSILVFFVSELVGGFGIAIVFMNHYPLEKIGDPVWDGHC 330
Db 308 LAHWHTWYLATWFLFKDPVNMVYLVLSQAVCGNLAIVFSLNHNMPVISKEEAVDMD 367
QY 331 FSVQIHETMNIIRGIITDFFEGGLNYQIEHHLWPTLPRHNLTAVSQYVEQLCQKHNLPY 390
Db 368 FFTQIITGRDVHPLFANWETGGLNYQIEHHLFSPMRHNSKIQPAVETLCKKNVRY 427
QY 391 RNPDPHEGLVILLRLYLAFAKQPA-----GKA 421
Db 428 HTTGMEGTA-----EVSRLNEVSKAASKMGKA 456

RESULT 14
US-08-834-033A-6
; Sequence 6, Application US/08834033A
; GENERAL INFORMATION:
; APPLICANT: KNUZON, DEBORAH
; APPLICANT: MUKERJI, PRADIP
; APPLICANT: HUANG, YUNG-SHENG
; APPLICANT: THURMOND, JENNIFER
; APPLICANT: CHAUDHARY, SUNITA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
; OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LIMBACH AND LIMBACH, L.L.P.
; STREET: 2001 FERRY BUILDING
; CITY: SAN FRANCISCO
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834.033A
; FILING DATE: 11-APR-1997
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: WARD, MICHAEL R.
; REGISTRATION NUMBER: 38,651
; REFERENCE/DOCKET NUMBER: CGAB-300.USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 433-4150
; TELEFAX: (415) 433-8716
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-834-033A-6

Query Match 24.7%; Score 565; DB 12; Length 355;
Best Local Similarity 34.9%; Pred. No. 9e-52;
Matches 127; Conservative 58; Mismatches 145; Indels 34; Gaps 6;

QY 82 DFRKRLRELIATGMFDASPLWYSKISTTGLGLVGLFYMVOYQM-----YFAGVLLGM 136
Db 1 EVKRLRTLFLSGLGYDSSKAYAFKVSFNLICWGLSTVIVAKWGQSTLANVLISALLGL 60
QY 137 HYQOMGLSHDICHQPFKRNWNNVGLVFGNGLOGFSVTCWKDRHNAHSATNVQGH 196

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;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,985
; FILING DATE: 24-OCT-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/834,033
; FILING DATE: 11-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/833,610
; FILING DATE: 11-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: RAE-VENTER, BARBARA
; REGISTRATION NUMBER: 32,750
; REFERENCE/DOCKET NUMBER: CGNE.128.01US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 328-4400
; TELEFAX: (650) 328-4477
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 457 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-956-985-15

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Query Match      27.2%; Score 622; DB 13; Length 457;
Best Local Similarity 32.7%; Pred. No. 1e-57;
Matches 149; Conservative 76; Mismatches 174; Indels 56; Gaps 11;

QY  2 KSKRQALSPQLM--EQTYDVSAWVNFHPGGAEIENYQGRDATDAFMVHFQEAFLK 59
DB  23 EGKDAEAPFLMIIDNKVDYDREFVDPHPGGS-VILTHVGKGTDFDTHPEAAWETL- 81
QY  60 RMPKINPSELPQAAVNAEQEDF-----RKLEELIATGMFASPLWYSYKISTT 110
DB  81 -----ANFV---GDIDESDRDIKNDFFAAEVKRLTLFQSLGYDSSKAYYAFKVSFN 131
QY  111 LGLGVLYFLMVOYQ-----YFIGAVLGMHYQMGWLSHDICHOTFKNRNWNVLVL 165
DB  132 LCINGLSTVIVAKWGOTSTLANVLSAALLGLFWQCGGLAHDLHGHQVQDFRWGDLFGA 191
QY  166 VFGNGLGQFSVTCWKDRHNAHSATNVQGHDPDIDNLPPLAWSEDDVTRASPI----- 219
DB  192 FLGGVCGQFSSSWKDKHNTTHAAPNVHVEDPDIDTHPLTWSEHALEMFSVDPDELTR 251
QY  219 --SRKIQOQYFYFLVICILLREIFWCQCVLTVRSKDRDNQYRSQYK-----EAIG 270
DB  252 MWSRFVNLQNTWFFYFIFLSFARLSWGLQSLFVLP-----NGQAKPSSGARVPISLVEQLS 307
QY  271 LALHWTLKALFHLFFMPSILTSLLVFFVSELVGGGIAIVFVFNHYPLEKIGDPVWDGHG 330
DB  308 LAHWHTWYLATMFLFKDPVNMVLYFLVSOAVCGNLLAIVFSLNHNHMPVISEEAVDMD 367
QY  331 FSVGQIHTMNIIRGIITDWFGLNLYQIEHHLWPLTPRNLTAVSQVQEQLOKKNLPY 390
; Sequence 4, Application US/09377452

```

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;
; GENERAL INFORMATION:
; APPLICANT: KNUTSON, DEBORAH
; APPLICANT: MURKERJI, PRADIP
; APPLICANT: HUANG, YUNG-SHENG
; APPLICANT: THURMOND, JENNIFER
; APPLICANT: CHAUDHARY, SUNITA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
; OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LIMBACH & LIMBACH L.L.P.
; STREET: 2001 FERRY BUILDING
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/377,452
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: WARD, MICHAEL R.
; REGISTRATION NUMBER: 38,651
; REFERENCE/DOCKET NUMBER: CGAB 101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)433-4150
; TELEFAX: (415)433-8716
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 457 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-377-452-4

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Query Match      27.2%; Score 622; DB 17; Length 457;
Best Local Similarity 32.7%; Pred. No. 1e-57;
Matches 149; Conservative 76; Mismatches 174; Indels 56; Gaps 11;

QY  2 KSKRQALSPQLM--EQTYDVSAWVNFHPGGAEIENYQGRDATDAFMVHFQEAFLK 59
DB  23 EGKDAEAPFLMIIDNKVDYDREFVDPHPGGS-VILTHVGKGTDFDTHPEAAWETL- 81
QY  60 RMPKINPSELPQAAVNAEQEDF-----RKLEELIATGMFASPLWYSYKISTT 110
DB  81 -----ANFV---GDIDESDRDIKNDFFAAEVKRLTLFQSLGYDSSKAYYAFKVSFN 131
QY  111 LGLGVLYFLMVOYQ-----YFIGAVLGMHYQMGWLSHDICHOTFKNRNWNVLVL 165
DB  132 LCINGLSTVIVAKWGOTSTLANVLSAALLGLFWQCGGLAHDLHGHQVQDFRWGDLFGA 191
QY  166 VFGNGLGQFSVTCWKDRHNAHSATNVQGHDPDIDNLPPLAWSEDDVTRASPI----- 219
DB  192 FLGGVCGQFSSSWKDKHNTTHAAPNVHVEDPDIDTHPLTWSEHALEMFSVDPDELTR 251
QY  219 --SRKIQOQYFYFLVICILLREIFWCQCVLTVRSKDRDNQYRSQYK-----EAIG 270
DB  252 MWSRFVNLQNTWFFYFIFLSFARLSWGLQSLFVLP-----NGQAKPSSGARVPISLVEQLS 307
QY  271 LALHWTLKALFHLFFMPSILTSLLVFFVSELVGGGIAIVFVFNHYPLEKIGDPVWDGHG 330
DB  308 LAHWHTWYLATMFLFKDPVNMVLYFLVSOAVCGNLLAIVFSLNHNHMPVISEEAVDMD 367
QY  331 FSVGQIHTMNIIRGIITDWFGLNLYQIEHHLWPLTPRNLTAVSQVQEQLOKKNLPY 390
; Sequence 4, Application US/09377452

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RESULT 12

US-09-377-452-4

; Sequence 4, Application US/09377452

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;
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 457 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-363-574-2

Query Match      27.6%   Score 631;   DB 17;   Length 457;
Best Local Similarity 33.0%;   Pred. No. 1.1e-58;
Matches 150;   Conservative 76;   Mismatches 173;   Indels 56;   Gaps 11;

QY  2 KSKQALSPQLM--EQTYDYSANVNFHPGGAETIENYQGRDATDAFMMHFQEAFLK 59
DB  23 EGKDAEAPFLMIIDNKVDYREFVDPHGG--VILTHVGKDGTDVDFTFPEAAWETL- 81
QY  60 RMPKINPSPFLPQAAVNEAQEDF-----RKLREELIATGMFASPLWYSKISTT 110
DB  81 -----ANFYV---GDIDESDRDIKNDDFAAEVVKRLTLFQSLGYDSSKAYIAFKVSFN 131
QY  111 LGLGVLYFLMVOYOM-----YFIGAVLLGMHYQOMGWLSDICHCHOTFKRNNNNLVGL 165
DB  132 LCITWGLSTVIVAKWGQSTLANVLNSAALLGLFWQCGWLAHDFLHQVQDFRFGDLFGA 191
QY  166 VFGNGLOGFSVTCWKDRNNAHSAATNVQGHDPDIDNLPPLAWSDDVTRASPI----- 219
DB  192 FLGGVCGCFSSWWKDKHNTHAAPNVHGEDPDIDTHTPLTWSEHALEMFSVDPDELTR 251
QY  219 --SRKLIQFOQYFLVICILLRFTWCFCQVLTVRSKDRNQFYSYKK-----BAIG 270
DB  252 MWSRFVNLQNTWFFPILSFARLSWCLQSILFVLP-----NGQAHKPSGARVPISLVEQLS 307
QY  271 LALHWTLKALFLHFLFMPISILTSLLVFFVSELVGGFGIAIVFMNHYPLEKIGDPVWDG 330
DB  308 LAMHTWYLATMFLFIKDPVNMVLYFLVSAVCGNLLAIVFSLNHNMPVISKEEAVDMD 367
QY  331 FSVGQIHTMNIIRGIITDWFQGLNYQIEHHLWPTLPRNHLTAVSQVQLCKHNL 390
DB  368 FFTKQIITGRDVHPGLFANFTGGLNYQIEHHLFSPNPRHNSKIQPAVETLCKKNVRY 427
QY  391 RNPPLPHEGLVILLRYLAVFARMAEKOPA-----GKA 421
DB  428 HTGMIEGTA-----EVFSRLNEVSKAASKMGKA 456

RESULT 10
US-08-834-033A-14
; Sequence 14, Application US/08834033A
; GENERAL INFORMATION:
; APPLICANT: KNOTZON, DEBORAH
; APPLICANT: MUKERJI, PRADIP
; APPLICANT: HUANG, YUNG-SHENG
; APPLICANT: THURMOND, JENNIFER
; APPLICANT: CHAUDHARY, SUNITA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
; TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LIMBACH AND LIMBACH, L.L.P.
; STREET: 2001 FERRY BUILDING
; CITY: SAN FRANCISCO
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:

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;
; APPLICATION NUMBER: US/08/834_033A
; FILING DATE: 11-APR-1997
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: WARD, MICHAEL R.
; REGISTRATION NUMBER: 38,651
; REFERENCE/DOCKET NUMBER: CGAB-300, USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 433-4150
; TELEFAX: (415) 433-8716
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 457 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-834-033A-14

Query Match      27.2%   Score 622;   DB 12;   Length 457;
Best Local Similarity 32.7%;   Pred. No. 1e-57;
Matches 149;   Conservative 76;   Mismatches 174;   Indels 56;   Gaps 11;

QY  2 KSKQALSPQLM--EQTYDYSANVNFHPGGAETIENYQGRDATDAFMMHFQEAFLK 59
DB  23 EGKDAEAPFLMIIDNKVDYREFVDPHGG--VILTHVGKDGTDVDFTFPEAAWETL- 81
QY  60 RMPKINPSPFLPQAAVNEAQEDF-----RKLREELIATGMFASPLWYSKISTT 110
DB  81 -----ANFYV---GDIDESDRDIKNDDFAAEVVKRLTLFQSLGYDSSKAYIAFKVSFN 131
QY  111 LGLGVLYFLMVOYOM-----YFIGAVLLGMHYQOMGWLSDICHCHOTFKRNNNNLVGL 165
DB  132 LCITWGLSTVIVAKWGQSTLANVLNSAALLGLFWQCGWLAHDFLHQVQDFRFGDLFGA 191
QY  166 VFGNGLOGFSVTCWKDRNNAHSAATNVQGHDPDIDNLPPLAWSDDVTRASPI----- 219
DB  192 FLGGVCGCFSSWWKDKHNTHAAPNVHVEDPDIDTHTPLTWSEHALEMFSVDPDELTR 251
QY  219 --SRKLIQFOQYFLVICILLRFTWCFCQVLTVRSKDRNQFYSYKK-----BAIG 270
DB  252 MWSRFVNLQNTWFFPILSFARLSWCLQSILFVLP-----NGQAHKPSGARVPISLVEQLS 307
QY  271 LALHWTLKALFLHFLFMPISILTSLLVFFVSELVGGFGIAIVFMNHYPLEKIGDPVWDG 330
DB  308 LAMHTWYLATMFLFIKDPVNMVLYFLVSAVCGNLLAIVFSLNHNMPVISKEEAVDMD 367
QY  331 FSVGQIHTMNIIRGIITDWFQGLNYQIEHHLWPTLPRNHLTAVSQVQLCKHNL 390
DB  368 FFTKQIITGRDVHPGLFANFTGGLNYQIEHHLFSPNPRHNSKIQPAVETLCKKNVRY 427
QY  391 RNPPLPHEGLVILLRYLAVFARMAEKOPA-----GKA 421
DB  428 HTGMIEGTA-----EVFSRLNEVSKAASKMGKA 456

RESULT 11
US-08-956-985-15
; Sequence 15, Application US/08956985
; GENERAL INFORMATION:
; APPLICANT: KNOTZON, DEBORAH
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
; TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
; STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94306

```

```

Db 81 -----ANFYV---GDIDESDRDKNDDFAAEVRKLRTLFQSLGYDSSKAYIAFKVSFN 131
Qy 111 LGLGVLYFLMVQYOM-----YFIGAVLLGMHYOQMGWLSHDICHQHTQFKNRNNLVGL 165
Db 132 LCTWGLSTVIYAKWGQSTLANVLSAALLGLFWQCGWLAHDFLHQVQDFRFGDLEGA 191
Qy 166 VFGNGLOGFSVTCWKORHNAHSATNVQGHDPDIDNPLPLAWSDEDDVTRASPI----- 219
Db 192 FLGVCVCGFSSWKKHNTHAAPNVHGEDPDIDTHPLTWSEHALEMFSVPDEELTR 251
Qy 219 --SRKLQFOQYFLVLCILLRFTWCFCQVLTVRSKDRDNQFYSQYKK-----BAIG 270
Db 252 MWSRFVNLQWTFYFPLSFARLSQCLQSLFVLP-----NGQAHKPGSGARVPSISLVEOLS 307
Qy 271 LAHWTALKALFLHFFMPSILTSLLVFFVSELVGGFIAVVMHNYPLEKIDPVDWGHG 330
Db 308 LAHWTWYLATMFLFIKDPVNMVLYFLVSQAVCGNLLAIVFSLNHNHGMPIVSKKEAVDMD 367
Qy 331 FSVGQIHETNIRGIIITDWFEGGLNYOIEHHLWPTLPRHNLTAVSQVOEQOLCKHNLPL 390
Db 368 FFTQKITGRDVHPGLFANWFTGGLNYOIEHHLFSPMRHNFESKIQPAVETLCKKYNRY 427
Qy 391 RNPLPHEGLVILLRYLAVFARMAEKQPA-----GKA 421
Db 428 HTTGMIEGTA-----EVFSRLNEVSKAASKMGKA 456

RESULT 8
US-09-363-526-2
; Sequence 2, Application US/09363526
; GENERAL INFORMATION:
; APPLICANT: KNUTZON, DEBORAH
; APPLICANT: MURKERJI, PRADIP
; APPLICANT: HUANG, YUNG-SHENG
; APPLICANT: THURMOND, JENNIFER
; APPLICANT: CHAUDHARY, SUNITA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
; TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LIMBACH AND LIMBACH L.L.P.
; STREET: 2001 FERRY BUILDING
; CITY: SAN FRANCISCO
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/363,526
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: WARD, MICHAEL R.
; REGISTRATION NUMBER: 38,651
; REFERENCE/DOCKET NUMBER: CGAB-201 USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 433-4150
; TELEFAX: (415) 433-8716
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 457 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-363-526-2

```

```

Query Match 27.68; Score 631; DB 17; Length 457;
Best Local Similarity 33.04; Pred. No. 1.le-58;
Matches 150; Conservative 76; Mismatches 173; Indels 56; Gaps 11;

Qy 2 KSKRQALSPLQLM--EOTYDVSAMVNFHPGGAETIENVQGRDATDAFVMVHFQEAFLK 59
Db 23 EGKADAPFLMIITDNKYVDVREFVDPHGGG-VILTHVGKDGTDVFTTFPEAAWETL- 81
Qy 60 RMPKINPSFELPPQAAVNEAQEDF-----RKLREELIATGMFASPLWYSYKISTT 110
Db 81 -----ANFYV---GDIDESDRDKNDDFAAEVRKLRTLFQSLGYDSSKAYIAFKVSFN 131
Qy 111 LGLGVLYFLMVQYOM-----YFIGAVLLGMHYOQMGWLSHDICHQHTQFKNRNNLVGL 165
Db 132 LCTWGLSTVIYAKWGQSTLANVLSAALLGLFWQCGWLAHDFLHQVQDFRFGDLEGA 191
Qy 166 VFGNGLOGFSVTCWKORHNAHSATNVQGHDPDIDNPLPLAWSDEDDVTRASPI----- 219
Db 192 FLGVCVCGFSSWKKHNTHAAPNVHGEDPDIDTHPLTWSEHALEMFSVPDEELTR 251
Qy 219 --SRKLQFOQYFLVLCILLRFTWCFCQVLTVRSKDRDNQFYSQYKK-----BAIG 270
Db 252 MWSRFVNLQWTFYFPLSFARLSQCLQSLFVLP-----NGQAHKPGSGARVPSISLVEOLS 307
Qy 271 LAHWTALKALFLHFFMPSILTSLLVFFVSELVGGFIAVVMHNYPLEKIDPVDWGHG 330
Db 308 LAHWTWYLATMFLFIKDPVNMVLYFLVSQAVCGNLLAIVFSLNHNHGMPIVSKKEAVDMD 367
Qy 331 FSVGQIHETNIRGIIITDWFEGGLNYOIEHHLWPTLPRHNLTAVSQVOEQOLCKHNLPL 390
Db 368 FFTQKITGRDVHPGLFANWFTGGLNYOIEHHLFSPMRHNFESKIQPAVETLCKKYNRY 427
Qy 391 RNPLPHEGLVILLRYLAVFARMAEKQPA-----GKA 421
Db 428 HTTGMIEGTA-----EVFSRLNEVSKAASKMGKA 456

RESULT 9
US-09-363-574-2
; Sequence 2, Application US/09363574
; GENERAL INFORMATION:
; APPLICANT: KNUTZON, DEBORAH
; APPLICANT: MURKERJI, PRADIP
; APPLICANT: HUANG, YUNG-SHENG
; APPLICANT: THURMOND, JENNIFER
; APPLICANT: CHAUDHARY, SUNITA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
; TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LIMBACH AND LIMBACH L.L.P.
; STREET: 2001 FERRY BUILDING
; CITY: SAN FRANCISCO
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/363,574
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: WARD, MICHAEL R.
; REGISTRATION NUMBER: 38,651
; REFERENCE/DOCKET NUMBER: CGAB-202 USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 433-4150
; TELEFAX: (415) 433-8716

```

	Matches	150;	Conservative	76;	Mismatches	173;	Indels	56;	Gaps	11;
Qy	2	KSKRALSPQLM	--EOTYDVSAMVNFHPGGAETIENYQGRDATDAEFMMHFQAFDKLK	59						
Db	23	EGKKDAEAPFLMIIDNKVYDREVPDPGGG-VILTHVGKDGTDVDTFHPAEAWEFL-81								
Qy	60	RMPKINSEELPPQAAVNAEQEDF-----RKLREELIATGMFDASPLWYSYKKTSTT	110							
Db	81	-----ANFYV-----GDIDESDRDKNDFAEVRKRLTLFOSLGYDSSKAYYAFKVSFN	131							
Qy	111	LGGLVGYFLMVOYOM-----YFIGAVLLGHYQOMGWLSDICHCHTTFKRNRNWNNVL	165							
Db	132	LCINGLSTVIYAKWGQSTTLANVLSAALLGLFWQCQGLAHDFLHHQVFOQDFRGWDLFGA	191							
Qy	166	VFGNGLOGFSVTCCHKDRNNAHSHATNYOGHPDDIDNLPPLAWSDDVTRASPI-----	219							
Db	192	FLGVCVCGE SSSWWKKDHNTTHAAAPNVHGEDDIDTTPHLLTWSHALEMFSDVPDEELTR	251							
Qy	219	--SRKLTFOQYYFLVCIILLREFWCFCQVLTVRSLLDRDNQFVSQYKK-----EAIG	270							
Db	252	MWSREMYLNTWTFYFPILSPARLSKCLQSILFVLP---NQCAHKPSGARVPISLVQSL	307							
Qy	271	LALHWTLKALFHLFFMPSIITSLVFFVSELVGGFGIAVYVFMNHYPLEKIDGVPWDGHC	330							
Db	308	LAMHWTYLATMFLFIKDPNVMNLVYFLVSQVCNLLAIYFSLNHNMGMPVTSKEEAVDMD	367							
Qy	331	FSVGOIHETWNIRRGIIITDFFEGGLNQIEHHLWPTLPRLNLTAVSYOVQOLCKHNLPY	390							
Db	368	FFYKQIITGRDVPGLFANWFTGGLNQIEHLEFSPSPRHNFYSKIQPAVETLCKKYNRY	427							
Qy	391	RNPLPHEGLVILRYLAVFARMAEKQPA-----GKA	421							
Db	428	HTTGMIEGTA-----EVFSRLNEVSKAASKMGA	456							

RESULT 6
US-09-087-578-4
; Sequence 4, Application US/09087578
; GENERAL INFORMATION:
; APPLICANT: KOPCHIK, JOHN J.
; APPLICANT: KELDER, BRUCE
; APPLICANT: HUANG, YUNG-SHENG
; APPLICANT: KIRCHNER, STEPHEN J.
; APPLICANT: MUKERJI, PRADIP
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: SYNTHESIS OF FATTY ACIDS, THEIR DERIVATIVES AND DOWNSTREAM
; TITLE OF INVENTION: PRODUCTS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL, LLP
; STREET: 220 MONTGOMERY STREET, SUITE 2200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/087,578
; FILING DATE: 29-MAY-1998
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: CARROLL, PETER G.
; REGISTRATION NUMBER: 32,837
; REFERENCE/DOCKET NUMBER: OHU-03348
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:

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; LENGTH: 457 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
US-09-087-578-4

Query Match          27.6%; Score 631; DB 14; Length 457;
Best Local Similarity 33.0%; Pred. No. 1.1e-58;
Matches 150; Conservative 76; Mismatches 173; Indels 56; Gaps 11

QY      2 KSKRQALSPLOLM--EQTYDYSAMVNHHPGGAETIENYQGRDATDAFWMVHFQFAFDKLUK 59
Db      23 EGKKDAEAPFLMIIDNKVYDREVFDPHGGG-VILTHVGKDGTDVFTFHPEAAWETL- 81

QY      60 RMPKINFSFELPPOAAVNAEQEDF-----RKRLRELIATGMFDPASPLWYSYKISTT 110
Db      81 -----ANFYV--GDIDESDRIDKNDFAAEVRKRLTLFQSLGYDSDSKAYYAEKVSFN 131

QY      111 LGLGVLYGYFLMVQVQM-----YFTGAVLLGMHYQOMGWLSHDICHQHTFKNNRNWNLVGL 165
Db      132 LCINGLSVTIVAKWGQSTSTLANVLSAALLGFWQCQGWLAHDFLHHQVFQDRFWGDLFGA 191

QY      166 VFGNGLGQSVTCVKDRHNAHSHATNYOGHPDPDIDNLPLPLAWSDDDDVTTRASPI----- 219
Db      192 FLGVCVCGGFSWWKDKHNTTHAAPNVHGEDPFDIDTHTPLLTWSHALEMFSDVDPDELTR 251

QY      219 --SRKLIQFOQYYELVICILLRFWICFQCVLTVTRSLKDRDNQFYRSQYKK-----EAIG 270
Db      252 MWSRFVNLQNTWTFYFPIILSPARLSWCLQSILFVLP---NGQAHKPSGARVPISLVEQLS 307

QY      271 LALHWTLKALFHLFFMFSSILTSLLVFFVSELVGGFGTAIVVFMNHYPLEKIGDPVWDGHG 330
Db      308 LAHWWTYLATMFLFIKDPVNMVLYFLVQAVCGNLLAIVFSLNHNHGMPIVSKEEAVDMD 367

QY      331 FSVGQIHETNWRIGIITDFFGGLNQIIEHLWPTLPRHNLTAVSYQVEOLCCKHNPLPY 390
Db      368 FFTQKIITGRDVPGLFANFTGGLNQIIEHLFSPRHRNFSKIQPAVELTCKKNYRVY 427

QY      391 RNPDPHEGLVILLRYLAVFARMAEKQPA-----GKA 421
Db      428 HTTGMIEGTA-----EVFSRLNEVSKAAKMGKA 456

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RESULT      7
US-09-351-525-4
; Sequence 4, Application US/09351525
; GENERAL INFORMATION:
; APPLICANT: Kopchick, John J.
; APPLICANT: Kelder, Bruce
; TITLE OF INVENTION: Mammalian Cells Expressing Desaturases and Elongases
; FILE REFERENCE: OHU-03765
; CURRENT APPLICATION NUMBER: US/09/351,525
; CURRENT FILING DATE: 1999-12-22
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 457
; TYPE: PRT
; ORGANISM: Mortierella Alpina
US-09-351-525-4

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Query Match      27.6%; Score 631; DB 17; Length 457;
Best Local Similarity 33.0%; Pred. No. 1.1e-58;
Matches 150; Conservative 76; Mismatches 173; Indels 56; Gaps 11;

QY      2 KSKRQALSPQLQM--EQTYDVSAAWNFHPGGABIIINYGRDATAFMVNHFQEAQDKLK 59
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      23 EGKKDAEAPFLMIIDNKVYDFEVPDHPGGS-VILTHVGKDGTDVDFTHPEAAAWETL- 81
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      60 RMPKINPSFELPPQAAVNEAQEDF-----RKUREELIATGMEDASPLWYSYKISTT 110
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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Db 308 LAMHTWYLATWELFIKDPVNLVFLVSOAVCGNLLAIVFSLNHNMPVISEEAVDMD 367
 Qy 331 FSVGOIHETMNRRIITDWFEGGLNYQIEHHLWPTLPRLHNTAVSYQVEQLCQKHNLPY 390
 Db 368 FFTKQITGRDHPGLFANFTGGLNYQIEHHLFSPMRHNSFKIOPAVETLCKKYNVRY 427
 Qy 391 RNPHEGLVILLRYLAVFARMAEKOPA-----GKA 421
 Db 428 HTGMIEGTA-----EVFSRLNEVSKAASKMGKA 456

RESULT 4
 US-08-956-985-2
 ; Sequence 2, Application US/08956985
 ; GENERAL INFORMATION:
 ; APPLICANT: KNUTZON, DEBORAH
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
 ; TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS
 ; NUMBER OF SEQUENCES: 28
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
 ; STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039
 ; CITY: PALO ALTO
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94306
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC Compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION NUMBER: US/08/956,985
 ; FILING DATE: 24-OCT-1997
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/834,033
 ; FILING DATE: 11-APR-1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/833,610
 ; FILING DATE: 11-APR-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: RAE-VENTER, BARBARA
 ; REGISTRATION NUMBER: 32,750
 ; REFERENCE/DOCKET NUMBER: CGNE.128.01US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (650) 328-4400
 ; TELEFAX: (650) 328-4477
 ; TELEX: N/A
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 457 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: not relevant
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-956-985-2

Query Match 27.6%; Score 631; DB 13; Length 457;
 Best Local Similarity 33.0%; Pred. No. 1.le-58;
 Matches 150; Conservative 76; Mismatches 173; Indels 56; Gaps 11;

Qy 2 KSKROALSLPLM--EQTVDYSAWVNFHPCGAEIENYQGRDATDAFMVHFOEAPDKLX 59
 Db 23 EGKKAEPFLMIDNKVDYVREFPDHPGGS-VILTHVGKGDVDVDTTHPEAAWTL- 81
 Qy 60 RMPKINPSPQLPQAANVEAQEDF-----RKREELIATGMFASPLWYSKIYSTT 110
 Db 81 -----ANFVV---GDIDESDRIKNDFFAAEVRKRLTLFQSLGYDSSKAYIAKVSFN 131
 Qy 111 LGIGVLGYFLMVOYQM-----YFIGAVLLGNHYQOMGLSHDCHHOTTFRNNWNLVL 165

Db 132 LCINGLSTVIVAKWGOTSTLANVLSAALLGLFWQCGWLAHDFLHHQVDFQDFRWDLFGA 191
 Qy 166 VFGNGLOQSVTCWDRHNAHSAATNVQGHDPDIDNLPLAWSEDDYTRASPI----- 219
 Db 192 FLGGVCOGFSSSWMDKHNTHAAPNVHGEDPDIDTHPLTWSEHALEMFSVDYDDELTR 251
 Qy 219 --SRKLIQFOQXYELVICILLRFIMCFQCVLTVRSLKDRDNQFYRQYKK-----EAIG 270
 Db 252 MMSRFVNLQNTWFFYFPIFLSARLSWCLQSLILFLP-----NGQAHKSGARVPISLVEQLS 307
 Qy 271 LALHWTLKALFHLFFEMPSILTSLLVFFVSELVGGFGIAIVFNMHYPLEXIGDPVWDGHC 330
 Db 308 LAMHTWYLATWELFIKDPVNLVFLVSOAVCGNLLAIVFSLNHNMPVISEEAVDMD 367
 Qy 331 FSVGOIHETMNRRIITDWFEGGLNYQIEHHLWPTLPRLHNTAVSYQVEQLCQKHNLPY 390
 Db 368 FFTKQITGRDHPGLFANFTGGLNYQIEHHLFSPMRHNSFKIOPAVETLCKKYNVRY 427
 Qy 391 RNPHEGLVILLRYLAVFARMAEKOPA-----GKA 421
 Db 428 HTGMIEGTA-----EVFSRLNEVSKAASKMGKA 456

RESULT 5
 US-08-956-985A-2
 ; Sequence 2, Application US/08956985A
 ; GENERAL INFORMATION:
 ; APPLICANT: KNUTZON, DEBORAH
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
 ; TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS
 ; NUMBER OF SEQUENCES: 28
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
 ; STREET: P.O. BOX 60039
 ; CITY: PALO ALTO
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94306-0039
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC Compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION NUMBER: US/08/956,985A
 ; FILING DATE: 24-OCT-1997
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/834,033
 ; FILING DATE: 11-APR-1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/833,610
 ; FILING DATE: 11-APR-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: RAE-VENTER, BARBARA
 ; REGISTRATION NUMBER: 32,750
 ; REFERENCE/DOCKET NUMBER: CGNE128.01US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (650) 328-4400
 ; TELEFAX: (650) 328-4477
 ; TELEX: N/A
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 457 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: not relevant
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-956-985A-2

Query Match 27.6%; Score 631; DB 13; Length 457;
 Best Local Similarity 33.0%; Pred. No. 1.le-58;


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Db 181 DRNAHRSATNVCHDHPDIDNLPPLAWSDDVTRASPISRRKLIQFQQYFLVICILLRFI 240
QY 241 WCFQCVLTVRSKDRDNQFVRSQYKKEAIGLALHWTALKALFLHFMPSILTSLLVFFVSE 300
Db 241 WCFQCVLTVRSKDRDNQFVRSQYKKEAIGLALHWTALKALFLHFMPSILTSLLVFFVSE 300
QY 301 LVGGFGIAIVFNMNHYPLEKIGDPVWDGHSVGOIHETNMIRGIIITDWFEGGLNYQIE 360
Db 301 LVGGFGIAIVFNMNHYPLEKIGDPVWDGHSVGOIHETNMIRGIIITDWFEGGLNYQIE 360
QY 361 HHLWPTLPRNLTAHSVQVQEQLCQKHNLPYRNPLPHEGLVILLRYLAVFAARMAEKOPAGK 420
Db 361 HHLWPTLPRNLTAHSVQVQEQLCQKHNLPYRNPLPHEGLVILLRYLAVFAARMAEKOPAGK 420
QY 421 AL 422
Db 421 AL 422

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RESULT 2
PCT-US99-28655-2
; Sequence 2, Application PC/TUS9928655
; GENERAL INFORMATION:
; APPLICANT: Browne, John et al.
; TITLE OF INVENTION: Desaturases and Methods of Using Them for Synthesis of
; FILE REFERENCE: 53860
; CURRENT APPLICATION NUMBER: PCT/US99/28655
; EARLIER FILING DATE: 1999-12-06
; EARLIER FILING DATE: 60/111,301
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
PCT-US99-28655-2

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Query Match 28.0%; Score 638.5; DB 1; Length 447;
Best Local Similarity 37.1%; Pred. No. 1.6e-59;
Matches 145; Conservative 64; Mismatches 151; Indels 31; Gaps 9;

QY 27 HPGGAELIENYQGRDATDAFWMH--FOEAFDKLKPMPKINPSF--ELP-----PQAAVN 77
Db 30 HPGGS-AITTYKNMDATVFTHTGSKAYQWLTELKKECPQEPIDKDDPIKGID 88
QY 78 EA-----QEDFKRLREELIATGMDASPLWYSYKISTTGLGLVGLVFLMW 122
Db 89 DYNMGTENISEKRSQAQINSFTDLRMVRAEGLMDGSPLEYIKLLETITLFAYL-- 147
QY 123 QYOMTFI-GAVILGMHYQMGWLSHDCHHTQFKNRNWNLVGLVFGNGLQGSFVTCWKD 181
Db 147 QYHTYLPAILGVAQWGLWLIHEFAHQHQLFKRYNDLASYFVGNLQGSFSGGWE 206
QY 182 RINAHSATNVCHDHPDIDNLPPLAWSDDVTRASPIS--RKLIQFQQYFLVICILLRF 239
Db 207 QINVHAATNVVGRDGLDLPFYATVAEHLNYSQDSWVMTLFRQHVHTFMPFLRL 266
QY 240 IWCFCVLTVRSKDRDNQFVRSQYKKEAIGLALHWTALKALFLHFMPSILTSLLVFFVS 299
Db 267 SWLLASIFVSOMPHYDYIRNTAYIEQVGLSLHAW--SLGOLYFLPDWSTRIMFFLV 325
QY 300 ELVGGFGIAIVFNMNHYPLEKIGDPVWDGHSVGOIHETNMIRGIIITDWFEGGLNYQI 359
Db 326 HLVGGLLSHVYFNHYSVKEKALSSNINSVACIQIMTRNRPGRFIDLWGLGLNYOI 385
QY 360 EHLWPTLPRNLTAHSVQVQEQLCQKHNLPY 390
Db 386 EHLWPTLPRNLTAHSVQVQEQLCQKHNLPY 416

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RESULT 3
US-08-834-033A-2
; Sequence 2, Application US/08834033A
; GENERAL INFORMATION:
; APPLICANT: KNUTZON, DEBORAH
; APPLICANT: MUKERJI, PRADIP
; APPLICANT: HUANG, YUNG-SHENG
; APPLICANT: THURMOND, JENNIFER
; APPLICANT: CHAUDHARY, SUNITA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
; OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LIMBACH AND LIMBACH, L.L.P.
; STREET: 2001 FERRY BUILDING
; CITY: SAN FRANCISCO
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,033A
; FILING DATE: 11-APR-1997
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: WARD, MICHAEL R.
; REGISTRATION NUMBER: 38,651
; REFERENCE/DOCKET NUMBER: CGAB-300.USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 433-4150
; TELEFAX: (415) 433-8716
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 457 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-834-033A-2

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Query Match 27.6%; Score 631; DB 12; Length 457;
Best Local Similarity 33.0%; Pred. No. 1.1e-58;
Matches 150; Conservative 76; Mismatches 173; Indels 56; Gaps 11;

QY 2 KSKROALSPQLM--EQTYDVSAWVNFHPGGAEIENYQGRDATDAFWMHFOEAFDKL 59
Db 23 EGKKADEAPFLMIIDNKVYDREVPDPHGG--VILTHVKGKDTVDFTFHPAAWETL- 81
QY 60 RMPKINPSELPPQAAVNEAQEDF-----RKLREELIATGMDASPLWYSYKIST 110
Db 81 -----ANFY---GDIDESDRDIXNDFFAAEVRKRLTLFQSLGYDSSKAYAFKVSFN 131
QY 111 LGLVGLVGLVVOYQM-----YFIGAVALGMHYQMGWLSHDCHHTQFKNRNWNLVGL 165
Db 132 LCINGLSIVIAKQWSTLANVLSNALLGLFWQCGGLAHDFLHHQVQDFRFGDLFGA 191
QY 166 VEGNGLQGSFVTCWKDRHNAHSATNVQGHDPDIDNLPPLAWSDDVTRASPIS----- 219
Db 192 FLGGVCGQGSFSSWKDKKNTTHAAPNVHGEDPDIDHPLLTWSEHALENFSDVDPDELTR 251
QY 219 --SRKLIQFQQYFLVICILLRFIWCFCVLTVRSKDRDNQFVRSQYKKE-----EATG 270
Db 252 MNSRFVNLNQTWTFYFPIILSFARLSWCLQSILFVLP---NGQAHKPSGARVPISLVEQLS 307
QY 271 LALHWTALKALFLHFMPSILTSLLVFFVSELVGGFGIAIVFNMNHYPLEKIGDPVWDGHS 330

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GenCore version 4.5
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OW protein - protein search, using sw model

Run on: February 25, 2000, 04:47:15 ; Search time 78.22 Seconds
(without alignments)
548.480 Million cell updates/sec

Title: PCT-US99-28655-4
Perfect score: 2283
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Scoring table: BLOSUM62

Searched: 645694 seqs, 101663753 residues

Database : Pending_Patents_AA:*

Word size : 0

Number of hits that pass the threshold : 645694
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2: /cgn2_6/ptodata/2/paa/US07_COMB.pep.*
3: /cgn2_6/ptodata/2/paa/US080_COMB.pep.*
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13: /cgn2_6/ptodata/2/paa/US089_COMB.pep.*
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16: /cgn2_6/ptodata/2/paa/US092_COMB.pep.*
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20: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep.*
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22: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep.*
23: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep.*
24: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	2283	100.0	422	1 PCT-US99-28655-4
2	638.5	28.0	447	1 PCT-US99-28655-2
3	631	27.6	457	12 US-08-834-033A-2
4	631	27.6	457	13 US-08-956-985-2
5	631	27.6	457	13 US-08-956-985A-2
6	631	27.6	457	14 US-09-087-578-4
7	631	27.6	457	17 US-09-351-525-4
8	631	27.6	457	17 US-09-363-526-2
9	631	27.6	457	17 US-09-363-574-2
10	622	27.2	457	12 US-08-834-033A-14
11	622	27.2	457	13 US-08-956-985-15
12	622	27.2	457	17 US-09-377-452-4
13	622	27.2	457	17 US-09-377-475-4
14	565	24.7	355	12 US-08-834-033A-6
15	565	24.7	355	13 US-08-956-985-7

16	565	24.7	355	13	US-08-956-985A-7	Sequence 7, Appli
17	565	24.7	355	17	US-09-363-526-5	Sequence 5, Appli
18	565	24.7	355	17	US-09-363-574-5	Sequence 5, Appli
19	498.5	21.8	458	15	US-09-116-639-5	Sequence 5, Appli
20	461	20.2	452	13	US-08-934-254-27	Sequence 27, Appli
21	443.5	19.4	445	14	US-09-048-888-1	Sequence 1, Appli
22	437.5	19.2	448	19	US-60-110-784-5	Sequence 5, Appli
23	433.5	19.0	448	13	US-08-934-254-5	Sequence 5, Appli
24	430.5	18.9	446	12	US-08-834-033A-15	Sequence 15, Appli
25	430.5	18.9	446	13	US-08-956-985-16	Sequence 16, Appli
26	430.5	18.9	446	13	US-08-956-985A-16	Sequence 16, Appli
27	430.5	18.9	446	17	US-09-377-452-5	Sequence 5, Appli
28	430.5	18.9	446	17	US-09-377-475-5	Sequence 5, Appli
29	430	18.8	444	14	US-09-048-888-3	Sequence 3, Appli
30	422	18.5	444	15	US-09-116-639-1	Sequence 1, Appli
31	416	18.2	444	17	US-09-351-525-8	Sequence 8, Appli
32	356	15.6	393	19	US-60-110-784-4	Sequence 4, Appli
33	302.5	13.3	286	19	US-60-110-784-9	Sequence 9, Appli
34	277.5	12.2	252	12	US-08-834-033A-8	Sequence 8, Appli
35	277.5	12.2	252	13	US-08-956-985-9	Sequence 9, Appli
36	277.5	12.2	252	13	US-08-956-985A-9	Sequence 9, Appli
37	277.5	12.2	252	17	US-09-363-526-7	Sequence 7, Appli
38	277.5	12.2	252	17	US-09-363-574-7	Sequence 7, Appli
39	249.5	10.9	446	12	US-08-834-033A-5	Sequence 5, Appli
40	249.5	10.9	446	13	US-08-956-985-6	Sequence 6, Appli
41	249.5	10.9	446	13	US-08-956-985A-6	Sequence 6, Appli
42	249.5	10.9	446	14	US-09-087-578-2	Sequence 2, Appli
43	249.5	10.9	446	15	US-09-145-828-23	Sequence 23, Appli
44	249.5	10.9	446	17	US-09-351-525-2	Sequence 2, Appli
45	249.5	10.9	446	17	US-09-377-452-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
PCT-US99-28655-4
; Sequence 4, Application PC/TUS9928655
; GENERAL INFORMATION:
; APPLICANT: Browne, John et al.
; TITLE OF INVENTION: Desaturases and Methods of Using Them for Synthesis of
; TITLE OF INVENTION: Polyunsaturated Fatty Acids
; FILE REFERENCE: 53860
; CURRENT APPLICATION NUMBER: PCT/US99/28655
; CURRENT FILING DATE: 1999-12-06
; EARLIER APPLICATION NUMBER: 60/111,301
; EARLIER FILING DATE: 1998-12-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Euglena gracilis
PCT-US99-28655-4

Query Match	100.0%	Score 2283;	DB 1;	Length 422;
Best Local Similarity	100.0%	Pred. No. 4.7e-236;		
Matches 422;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MKSKRQALSPQLMEQTYDVSAWNPHPGAGAEIENYQGRDATDAFNMVHFQAFDKLR	60	
Db	1	MKSKRQALSPQLMEQTYDVSAWNPHPGAGAEIENYQGRDATDAFNMVHFQAFDKLR	60	
QY	61	MPKINSFELPPQAAVNEAQEDFRKRLRELIATGMEDASPLWYSYKISTTLGLGVLGYEL	120	
Db	61	MPKINSFELPPQAAVNEAQEDFRKRLRELIATGMEDASPLWYSYKISTTLGLGVLGYEL	120	
QY	121	MVOYQMYFICAVLLGHYQMGWLSHDICHQTFKRNWNVNLVGLVFGNGLQGSFVTCWK	180	
Db	121	MVOYQMYFICAVLLGHYQMGWLSHDICHQTFKRNWNVNLVGLVFGNGLQGSFVTCWK	180	
QY	181	DRNHAHSATNVQGHDPDIDNPLPAWSEDDVTRASPISRKLIKQFOOQYFVLICILURFI	240	

QY 340 MNI-RGIIITDWFEGGLNYQIEHHLWPTLPRHNLTAVSQVEQLCKHNLPLY 391
 Db 284 ANFATNPNWNNFCGGLNHQVTHLFPNCHIHYPOLNIIKDVCQCFGVYK 336

RESULT 15
 US-08-833-610-7
 ; Sequence 7, Application US/08833610
 ; Patent No. 5972664
 ; GENERAL INFORMATION:
 ; APPLICANT: KUTZON, DEBORAH
 ; APPLICANT: MURKERJI, PRADIP
 ; APPLICANT: HUANG, YUNG-SHENG
 ; APPLICANT: THURMOND, JENNIFER
 ; APPLICANT: CHAUDHARY, SUNITA
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
 ; OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: RAE-VENTER LAW GROUP, P. C.
 ; STREET: 260 SHERIDAN AVE, P.O. BOX 60039
 ; CITY: PALO ALTO
 ; STATE: CALIFORNIA
 ; COUNTRY: USA
 ; ZIP: 94306
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/833,610
 ; FILING DATE: 11-APR-1997
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: RAE-VENTER, BARBARA
 ; REGISTRATION NUMBER: 32,750
 ; REFERENCE/DOCKET NUMBER: CGNE.123.00US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (650)328-4400
 ; TELEFAX: (650)328-4477
 ; TELEX: N/A
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 365 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: not relevant
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 US-08-833-610-7

Query Match 9.5%; Score 218; DB 2; Length 365;
 Best Local Similarity 23.6%; Pred. No. 2.1e-17;
 Matches 70; Conservative 55; Mismatches 110; Indels 62; Gaps 13;
 QY 126 MYFICAVLGLGMHYQMGW-LSHDICHHQTFKNNRW-NNLVGLVFGNGLOGESVTCWKDRH 183
 Db 68 MKLGGCVLGVGSVGVFNISHD-GNHGYSKYQWVNYLSGLT-HDAIGVSSYLMKFRH 124
 QY 184 NA-HHSATNVQGHDPDIDNPLAWSEDDVTRASPIS--RKLQFOQYFLVICILLRET 240
 Db 125 NYLHHTYTNILGHDEIHG-----DELVRMSPSMERYWYRHQHWFIWFYPIFY 176
 QY 241 WCFQCVLTVRSKDRNQYRSQYK-----EAIGLALHWTLKALFHL 283
 Db 177 W-----SIADVQTMLEKROYHDHEIPSTWVDIATLAFKAFGAVFLIPIAVGY 227
 QY 284 FPMPSILTSLLVFFSVLGGFGIAIVFWMNHYPLEKIG-----DPVWDGHHGFSVG 334
 Db 228 SPLVAVIGASIVYTHGLV-----ACVFMALAHVIEPAEFDPDNLHIDDEW-----ATA 277

QY 335 QIHETMNI-RGIIITDWFEGGLNYQIEHHLWPTLPRHNLTAVSQVEQLCKHNLPLY 390
 Db 278 QVKTIVDFAPNNTIINWYVGLNYQTVHHLFPHICHIHYPKIAPIAEVCEEFVNY 334

Search completed: February 25, 2000, 00:29:33
 Job time: 25091 sec

QY 340 MNI-RRGITDWFEGGLNYQIEHHLWPTLPRHNTAVSYQVQLCQKHNLPYR 391
 Db 284 ANFATNPNFNNWFCGGLNHQVTHLFPNICHIIHYPOLENIKDYCQDFGVYK 336

RESULT 13

US-08-789-936-2
 ; Sequence 2, Application US/08789936
 ; Patent No. 5789220
 ; GENERAL INFORMATION:
 ; APPLICANT: Thomas, Terry L.
 ; APPLICANT: Reddy, Avutu S.
 ; APPLICANT: Nuccio, Michael
 ; APPLICANT: Freyssinet, Georges L.
 ; APPLICANT: Nunberg, Andrew N.
 ; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
 ; TITLE OF INVENTION: DELTA 6-DESATURASE
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Scully, Scott, Murphy & Presser
 ; STREET: 400 Garden City Plaza
 ; CITY: Garden City
 ; STATE: New York
 ; COUNTRY: United States
 ; ZIP: 11530
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/789,936
 ; FILING DATE: 28-JAN-1997
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/366,779
 ; FILING DATE: 30-DEC-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Presser, Leopold
 ; REGISTRATION NUMBER: 19,827
 ; REFERENCE/DOCKET NUMBER: 83832YXW
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (516) 742-4343
 ; TELEFAX: (516) 742-4366
 ; TELEX: 230 901 SANS UR
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 359 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-789-936-2

Query Match 10.5%; Score 239; DB 1; Length 359;
 Best Local Similarity 24.9%; Pred. No. 6.5e-20;
 Matches 73; Conservative 58; Mismatches 126; Indels 36; Gaps 13;

QY 119 FLMVQYQMFYFAGVLLGMHYQQMGW-LSHDICHQHTFKNNNNLVGLVFGNGLQGFVSVT 177
 Db 60 FAPVFPVRLGCMVLAIALAAFSFNVGHDANHNAYSSNPHINRVLGMY--DFVGLSSF 117
 QY 178 CWKDRHN-AHHSATNVQGHDPDIDLPLAWSDDVTRASPISRK--LIQFOQYYFLVIC 234
 Db 118 LWRYRHNLYHTYTNILGHVDEIHG-----DGAVRMSPEQEHVYRFOQFYIWLGLY 169
 QY 235 ILLRFTW-CFQCVLTVRSKDRDNQF--YRSQYKKAIGALHWTIKALFHL-----FFM 286
 Db 170 LFIPFYWFYDYLVLNKGKHYDHKIPFPQPLELASLLGIKLLW-LGYVFGPLALGFSI 228
 QY 287 PSILTSLLVFFVSELVGGFGIAI-VVFMNHYPLEKIGDPVWDGCHG-----FSVGOIHET 339

Db 229 PEVLIGASVTYMT-----YGIIVCTIFMLAHVLESTFLLPDGSGAIDDEWAICQIRTT 283
 QY 340 MNI-RRGITDWFEGGLNYQIEHHLWPTLPRHNTAVSYQVQLCQKHNLPYR 391
 Db 284 ANFATNPNFNNWFCGGLNHQVTHLFPNICHIIHYPOLENIKDYCQDFGVYK 336

RESULT 14

US-08-833-610-6
 ; Sequence 6, Application US/08833610
 ; Patent No. 5972664
 ; GENERAL INFORMATION:
 ; APPLICANT: KUTZON, DEBORAH
 ; APPLICANT: MURKERJI, PRADIP
 ; APPLICANT: HUANG, YUNG-SHENG
 ; APPLICANT: THURMOND, JENNIFER
 ; APPLICANT: CHAUDHARY, SUNITA
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
 ; TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
 ; STREET: 260 SHERIDAN AVE, P.O. BOX 60039
 ; CITY: PALO ALTO
 ; STATE: CALIFORNIA
 ; COUNTRY: USA
 ; ZIP: 94306
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/833,610
 ; FILING DATE: 11-APR-1997
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: RAE-VENTER, BARBARA
 ; REGISTRATION NUMBER: 32,750
 ; REFERENCE/DOCKET NUMBER: CGNE.123.00US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (650)328-4400
 ; TELEFAX: (650)328-4477
 ; TELEX: N/A
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 359 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: not relevant
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-833-610-6

Query Match 10.5%; Score 239; DB 2; Length 359;
 Best Local Similarity 24.9%; Pred. No. 6.5e-20;
 Matches 73; Conservative 58; Mismatches 126; Indels 36; Gaps 13;

QY 119 FLMVQYQMFYFAGVLLGMHYQQMGW-LSHDICHQHTFKNNNNLVGLVFGNGLQGFVSVT 177
 Db 60 FAPVFPVRLGCMVLAIALAAFSFNVGHDANHNAYSSNPHINRVLGMY--DFVGLSSF 117
 QY 178 CWKDRHN-AHHSATNVQGHDPDIDLPLAWSDDVTRASPISRK--LIQFOQYYFLVIC 234
 Db 118 LWRYRHNLYHTYTNILGHVDEIHG-----DGAVRMSPEQEHVYRFOQFYIWLGLY 169
 QY 235 ILLRFTW-CFQCVLTVRSKDRDNQF--YRSQYKKAIGALHWTIKALFHL-----FFM 286
 Db 170 LFIPFYWFYDYLVLNKGKHYDHKIPFPQPLELASLLGIKLLW-LGYVFGPLALGFSI 228
 QY 287 PSILTSLLVFFVSELVGGFGIAI-VVFMNHYPLEKIGDPVWDGCHG-----FSVGOIHET 339
 Db 229 PEVLIGASVTYMT-----YGIIVCTIFMLAHVLESTFLLPDGSGAIDDEWAICQIRTT 283

Db 284 ANFATNPNFWFCGGLNHQVTHLFPNICHYPOLENIHKDVCOEFGVEYK 336

US-08-478-727-2

```

; Sequence 2, Application US/08478727
; Patent No. 5663068
; GENERAL INFORMATION:
; APPLICANT: Thomas, Terry L.
; APPLICANT: Reddy, Avutu S.
; APPLICANT: Nuccio, Michael
; APPLICANT: Freyssinet, Georges L.
; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC
; TITLE OF INVENTION: ACID BY A DELTA 6-DESATURASE
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,727
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/307,382
; FILING DATE: 14-SEP-1994
; APPLICATION NUMBER: US 07/817,919
; FILING DATE: 08-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: McNulty, William E.
; REGISTRATION NUMBER: 22,606
; REFERENCE/DOCKET NUMBER: 83832
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-478-727-2

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Query Match 10.5%; Score 239; DB 1; Length 359;
 Best Local Similarity 24.9%; Pred. No. 6.5e-20;
 Matches 73; Conservative 58; Mismatches 126; Indels 36; Gaps 13;

QY 119 FLWVQYMYFVIGAVLGMHYQQMGW--LSHDICHQHTFKNRNWNVLVGLVFGNGLOGFSVT 177
 DB 60 FAPVIPPVLLGCMVLAIAAFSEFNVGHDANHNAYSSNPHINRVLGMTY--DFVGLSSF 117
 QY 178 CWKDRHN-AHHSATNVQGHDPDIDNLPPLAWSDDVTRASPISRK--LQFOQYYFLVIC 234
 DB 118 LWRYRHNYLHTYTNILGHVDEIHG-----DGAVRMSPEQEHVGIYRFOQFYIWGLY 169
 QY 235 ILLRFTW-CFOCVLTVRSKDRDNQF--YRSQYKKEAIGLALHWTLKALFHL-----FFM 286
 DB 170 LPIPFYFVLYDVVLYLNKGYHDHKIPFPQPLELASLLGKLLW-LGYVFGPLALGFSI 228
 QY 287 PSILTSLLVFFVSELVGGFGIAI--VVFMMHYPLEKIGDPVWDGHC-----FSVGOIHET 339
 DB 229 PEVLIGASTYMT-----YGVVCTTFMLAHVLESTFELTPDGESGAIDDEWAICQIRTT 283
 QY 340 MNI-RRGIITDWFGLNLYQIEHHLWPTLPRNLNLTAVSYQVEQLCQKHNLNLYR 391

RESULT 12

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US-08-473-508-2
; Sequence 2, Application US/08473508
; Patent No. 5689050
; GENERAL INFORMATION:
; APPLICANT: Thomas, Terry L.
; APPLICANT: Reddy, Avutu S.
; APPLICANT: Nuccio, Michael
; APPLICANT: Freyssinet, Georges L.
; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC
; TITLE OF INVENTION: ACID BY A DELTA 6-DESATURASE
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/473,508
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/307,382
; FILING DATE: 14-SEP-1994
; APPLICATION NUMBER: US 07/817,919
; FILING DATE: 08-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: McNulty, William E.
; REGISTRATION NUMBER: 22,606
; REFERENCE/DOCKET NUMBER: 83832
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-473-508-2

```

Query Match 10.5%; Score 239; DB 1; Length 359;
 Best Local Similarity 24.9%; Pred. No. 6.5e-20;
 Matches 73; Conservative 58; Mismatches 126; Indels 36; Gaps 13;

QY 119 FLWVQYMYFVIGAVLGMHYQQMGW--LSHDICHQHTFKNRNWNVLVGLVFGNGLOGFSVT 177
 DB 60 FAPVIPPVLLGCMVLAIAAFSEFNVGHDANHNAYSSNPHINRVLGMTY--DFVGLSSF 117
 QY 178 CWKDRHN-AHHSATNVQGHDPDIDNLPPLAWSDDVTRASPISRK--LQFOQYYFLVIC 234
 DB 118 LWRYRHNYLHTYTNILGHVDEIHG-----DGAVRMSPEQEHVGIYRFOQFYIWGLY 169
 QY 235 ILLRFTW-CFOCVLTVRSKDRDNQF--YRSQYKKEAIGLALHWTLKALFHL-----FFM 286
 DB 170 LPIPFYFVLYDVVLYLNKGYHDHKIPFPQPLELASLLGKLLW-LGYVFGPLALGFSI 228
 QY 287 PSILTSLLVFFVSELVGGFGIAI--VVFMMHYPLEKIGDPVWDGHC-----FSVGOIHET 339
 DB 229 PEVLIGASTYMT-----YGVVCTTFMLAHVLESTFELTPDGESGAIDDEWAICQIRTT 283

Db 405 LAIKNTCEYKVPY 419

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RESULT 9
US-08-307-382-2
; Sequence 2, Application US/08307382
; Patent No. 5552306
; GENERAL INFORMATION:
; APPLICANT: Thomas, Terry L.
; APPLICANT: Reddy, Avutu S.
; APPLICANT: Nuccio, Michael
; APPLICANT: Freyssinet, Georges L.
; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC
; TITLE OF INVENTION: ACID BY A DELTA 6-DESATURASE
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/307,382
; FILING DATE: 14-SEP-1994
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/817,919
; FILING DATE: 08-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: McNulty, William E.
; REGISTRATION NUMBER: 22,606
; REFERENCE/DOCKET NUMBER: 8383Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4363
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-307-382-2

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Query Match 10.5%; Score 239; DB 1; Length 359;
Best Local Similarity 24.9%; Pred. No. 6.5e-20;
Matches 73; Conservative 58; Mismatches 126; Indels 36; Gaps 13;

QY 119 ELMVQYQMFYFVIGAVLGMHYQMGW-LSHDICHQHFKNRNNVNLGLVFGNGLQGFVSVT 177
Db 60 FAPVFPVLLGCMVLAIAALAAFSFNVGHDANHNAYSSNPHINRVLGMTY--DFVGLSSF 117
QY 178 CWKDRHN-AHHSATNVQGHDPDIDNLPPLAWSDDVTRASPISRK--LIQFOQYFVLV 234
Db 118 LMRYNHLYHHTYTNILGHVDEHG-----DGAVRMSPEQEHVGIYRFQFYTWGLY 169
QY 235 ILLRFTW-CFOCVLTVRSKDRDNQF--YRSQYKKEAIGLALHTLTKALFHL-----FFM 286
Db 170 LEIPFYWFYLDVYLVNKGKHYDHKIPPOPLELASLLGKLLW-LGYVFGPLALGFSI 228
QY 287 PSTLTSLLVFFVSELVGGFGIAI-VVFMNHYPLEKIGDPWDGCHG-----FVSGIHT 339
Db 229 PEVLIGASTYMT-----YGVVCTIFMLAHVLESTFTLPDGESGAIDDEWAICQIRT 283
QY 340 MNI-RRGIITDFFGGLNYQIEHHLWPTLPRHNLTAVSQVEQLCKQHNLPYR 391

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Db 284 ANFATNPNFNNWFCGLNHQVTHLFPNICHIPQLENIKDVCOEFGVEYK 336

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RESULT 10
US-08-366-779-2
; Sequence 2, Application US/08366779
; Patent No. 5614393
; GENERAL INFORMATION:
; APPLICANT: Thomas, Terry L.
; APPLICANT: Reddy, Avutu S.
; APPLICANT: Nuccio, Michael
; APPLICANT: Freyssinet, Georges L.
; APPLICANT: Nudberg, Andrew N.
; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
; TITLE OF INVENTION: DELTA 6-DESATURASE
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/366,779
; FILING DATE: 30-DEC-1994
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Presser, Leopold
; REGISTRATION NUMBER: 19,827
; REFERENCE/DOCKET NUMBER: 8383ZYXW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-366-779-2

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Query Match 10.5%; Score 239; DB 1; Length 359;
Best Local Similarity 24.9%; Pred. No. 6.5e-20;
Matches 73; Conservative 58; Mismatches 126; Indels 36; Gaps 13;

QY 119 ELMVQYQMFYFVIGAVLGMHYQMGW-LSHDICHQHFKNRNNVNLGLVFGNGLQGFVSVT 177
Db 60 FAPVFPVLLGCMVLAIAALAAFSFNVGHDANHNAYSSNPHINRVLGMTY--DFVGLSSF 117
QY 178 CWKDRHN-AHHSATNVQGHDPDIDNLPPLAWSDDVTRASPISRK--LIQFOQYFVLV 234
Db 118 LMRYNHLYHHTYTNILGHVDEHG-----DGAVRMSPEQEHVGIYRFQFYTWGLY 169
QY 235 ILLRFTW-CFOCVLTVRSKDRDNQF--YRSQYKKEAIGLALHTLTKALFHL-----FFM 286
Db 170 LEIPFYWFYLDVYLVNKGKHYDHKIPPOPLELASLLGKLLW-LGYVFGPLALGFSI 228
QY 287 PSTLTSLLVFFVSELVGGFGIAI-VVFMNHYPLEKIGDPWDGCHG-----FVSGIHT 339
Db 229 PEVLIGASTYMT-----YGVVCTIFMLAHVLESTFTLPDGESGAIDDEWAICQIRT 283
QY 340 MNI-RRGIITDFFGGLNYQIEHHLWPTLPRHNLTAVSQVEQLCKQHNLPYR 391
Db 284 ANFATNPNFNNWFCGLNHQVTHLFPNICHIPQLENIKDVCOEFGVEYK 336

```

APPLICANT: MURKERJI, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,655
FILING DATE: 11-APR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RAE-VENTER, BARBARA
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: CGNE.124.000S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 328-4400
TELEFAX: (650) 328-4477
TELEX: N/A
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 252 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-834-655-7

Query Match 12.2%; Score 277.5; DB 2; Length 252;
Best Local Similarity 29.3%; Pred. No. 1e-24;
Matches 80; Conservative 39; Mismatches 105; Indels 49; Gaps 10;
QY 114 GVLGYFLWQYQYFICAVLLGHYQMGWLSHDICHQTFKKNWNLVGLVFGNGLOG 173
DB 5 GYLACTSVFAHQ---IAAALLGLWIOSAYIGHDSGHYVMSKSYNRFQALLSGNCLTG 61
QY 174 FSVTCWKDRNNAHSATNVQGHDPDIDNLPPLAWSE-----DDVTRASPIRKL 222
DB 62 ISIAWKWTINAHNLACSLDYPDLQHIPVFAVSTKFFSLTSRFDYDRKLTGCPVAREL 121
QY 223 IQOQYQ-YFLVICI--LLRFIWCFCQVLTVRSLKDRDNQYRSQYKKEAIGLALHWTKA 279
DB 122 VSYQHTYYPVNCFGRLNFIQTFLFLSKREVPDRALNE-----AGILVFETWFP 172
QY 280 LF-----HLFFMPSILTSLLVFFVSELVGGFGTAIVFNMHYPLE-KIGDPVNDGH 329
DB 173 LLVSLPLNMPERFFF---VFTSFVTALQH-----IOFTLNHFAADVVGPPPT--GS 219
QY 330 GFSVGQIHTMNIIRRGIIITDFFGGLNYQIEHH 362
DB 220 DWFEKQAAGTIDISCRSYNDWFFGGLQFQLEHH 252
RESULT 8
US-08-833-610-2
Sequence 2, Application US/08833610
Patent No. 5972664
GENERAL INFORMATION:
APPLICANT: KNUTZON, DEBORAH
APPLICANT: MURKERJI, PRADIP

APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
STREET: 260 SHERIDAN AVE, P.O. BOX 60039
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,610
FILING DATE: 11-APR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RAE-VENTER, BARBARA
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: CGNE.123.000S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 328-4400
TELEFAX: (650) 328-4477
TELEX: N/A
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 446 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-833-610-2

Query Match 10.9%; Score 249.5; DB 2; Length 446;
Best Local Similarity 24.1%; Pred. No. 5.2e-21;
Matches 105; Conservative 68; Mismatches 167; Indels 95; Gaps 22;
QY 11 LQLEQTYDYSAWVNFHPGGAETIENYQGRDATDAFVMVHFOEAFDKLRMPKINP--SF 68
DB 25 LATRGVYDYTKLSRHPGGVDLLLCAGRDVTPVFEMYHAFGAADAIMKKYYVGLVSN 84
QY 69 ELP--POAAVNEAQEPRKLRLELIATGMF-----DASPLWYSYKISTTLGLGLVGY 118
DB 85 ELPIPEPTV-----FHKTIKTRV-EGYFTDRNIDPKNRPEIWRGVAL-----IFGS 130
QY 119 FLWVQYQYIIG-----AVLLGHYQMGWLS-HDICHQTFKKNWNLVGL 165
DB 131 LIASYYAQLEVPFVVERTWLVQVFAITMGFACQVGLNPLHDSHFVTHNPTVKILGA 190
QY 166 V--FGNGLQFSVTCWKDRN-AHHSATNVQGHDPDIDNLPPLAWSDDVTRASPIRKL 222
DB 191 THOFFNGA---SYLVWYQHWLGHHPYTNAGADPDVST-----SEPDVRIKPNQWF 241
QY 223 I-QFOQYFVLVICI--LLRFIWCFCQVLTVRSLKDRDNQYRSQYKKEAIGL-----A 272
DB 242 VNHQNHMFVFLYGLLAFKVRIOQINILYFVKTD-----AIRVNPISWTWHTV 290
QY 273 LHWTLKALF-----HLFFMPSILTSLLVFFVSELVGGFGTAIVFNMHYPLEKIGDPV 325
DB 291 MFWGGAFFVYRLLVPLQYLP-LGKVLLEFTVADVMYSSYVALTFOANH-VVEVQWPL 348
QY 326 WDGHG-----FVGQIHTMNIIRRG-----IITDFFGGLNYQIEHMLWTLPHRNLTA 375
DB 349 PDENGIIQKDWAAQVETQDYAHDLSLTSIT-----GSLNYQAVHLLFPNVSQHHPI 404
QY 376 SYQVEQLCKXHNLPY 390


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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/789,936
; FILING DATE: 28-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/366,779
; FILING DATE: 30-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Presser, Leopold
; REGISTRATION NUMBER: 19,827
; REFERENCE/DOCKET NUMBER: 8383YXW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 448 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE:
US-08-789-936-5

```

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Query Match      19.08; Score 433.5; DB 1; Length 448;
Best Local Similarity 29.8%; Pred. No. 7.6e-43;
Matches 121; Conservative 67; Mismatches 167; Indels 51; Gaps 14;

QY 11 LQLMEQTYDVSANVNFHFGGAEIENYQGRDATDAFVMVHFQAEADKLKRMKPKINPSFEL 70
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 25 ISTQKAYDVSQWVNDHPGSGFPLKSLAGQEVDAFVAFHPASTW---KNLDRFFTGYYL 81

QY 71 PPOAAVNEAQEDFRKLREELIATGMFDA-----SPLWYSYKISTTLGLVGLVGYFLMVQY 124
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 82 -KDYSEVSESKDYRKLVFEFSKMGLYDKKGHMFATLCF---IAMLFAMSVYGVLFCEGV 137

QY 125 QMYFICAVLGMHYQMGWLSHDCHQTFKRNWNNLVGLVFGNGLOGFSVTCWKDRHN 184
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 138 LVHLFSGCLMGFLWIOSGWIHGDAGHYVWVSDSLNKFNGIFAANCLSGISIGWKNHN 197

QY 185 AHSATNVQGHDPDIDNLPPLAWS-----EDDVTRASPIRKLIQOQYYFLV 232
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 198 AHIIACNSLEYDPLQIPIPLVYSSKFFGSLTSHFEYKRLTFDS--LSRFFVSQHWTFYP 256

QY 233 ICILLRFNCFQCVLTVRSKDRDNQFYRSQYKKEAIGLALHWTALKALHFLFPMPSILTS 292
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 257 IMCAARLNMYVQSLI---MLTKRNVSYRAQ---ELLGC-----LVFSIWY--PLLVS 301

QY 293 LL-----VFFVSELYGGFGIAIVVF-MNHYPLE-KIGDPVWDGCHGFSVGOIHETMNI 344
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 302 CLPNWGERIMFVIASVLTGMQVQFSLNHFSSSVYVGRP--KGNWFEKQTDGTLDISC 359

QY 345 GIITDWFGLNYQIEHHLWPTLPRHNLTAVSQVQEQLOCKHNL 390
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 360 PPWMDWFHGGLOFQIEHHLFPKMPRCNLRKISPYVIELCKHNL 405

```

```

RESULT 6
US-08-833-610-5
; Sequence 5, Application US/08833610
; Patent No. 5972664
; GENERAL INFORMATION:
; APPLICANT: KNUTZON, DEBORAH
; APPLICANT: MURKERJI, PRADIP
; APPLICANT: HUANG, YUNG-SHENG
; APPLICANT: THURMOND, JENNIFER
; APPLICANT: CHAUDHARY, SUNITA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
; TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS
; NUMBER OF SEQUENCES: 12

```

```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
; STREET: 260 SHERIDAN AVE, P.O. BOX 60039
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833,610
; FILING DATE: 11-APR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: RAE-VENTER, BARBARA
; REGISTRATION NUMBER: 32,750
; REFERENCE/DOCKET NUMBER: CGNE.123.00US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)328-4400
; TELEFAX: (650)328-4477
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 446 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-833-610-5

```

```

Query Match      18.9%; Score 430.5; DB 2; Length 446;
Best Local Similarity 29.8%; Pred. No. 1.7e-42;
Matches 121; Conservative 67; Mismatches 167; Indels 51; Gaps 14;

QY 11 LQLMEQTYDVSANVNFHFGGAEIENYQGRDATDAFVMVHFQAEADKLKRMKPKINPSFEL 70
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 25 ISTQKAYDVSQWVNDHPGSGFPLKSLAGQEVDAFVAFHPASTW---KNLDRFFTGYYL 81

QY 71 PPOAAVNEAQEDFRKLREELIATGMFDA-----SPLWYSYKISTTLGLVGLVGYFLMVQY 124
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 82 -KDYSEVSESKDYRKLVFEFSKMGLYDKKGHMFATLCF---IAMLFAMSVYGVLFCEGV 137

QY 125 QMYFICAVLGMHYQMGWLSHDCHQTFKRNWNNLVGLVFGNGLOGFSVTCWKDRHN 184
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 138 LVHLFSGCLMGFLWIOSGWIHGDAGHYVWVSDSLNKFNGIFAANCLSGISIGWKNHN 197

QY 185 AHSATNVQGHDPDIDNLPPLAWS-----EDDVTRASPIRKLIQOQYYFLV 232
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 198 AHIIACNSLEYDPLQIPIPLVYSSKFFGSLTSHFEYKRLTFDS--LSRFFVSQHWTFYP 256

QY 233 ICILLRFNCFQCVLTVRSKDRDNQFYRSQYKKEAIGLALHWTALKALHFLFPMPSILTS 292
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 257 IMCAARLNMYVQSLI---MLTKRNVSYRAQ---ELLGC-----LVFSIWY--PLLVS 301

QY 293 LL-----VFFVSELYGGFGIAIVVF-MNHYPLE-KIGDPVWDGCHGFSVGOIHETMNI 344
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 302 CLPNWGERIMFVIASVLTGMQVQFSLNHFSSSVYVGRP--KGNWFEKQTDGTLDISC 359

QY 345 GIITDWFGLNYQIEHHLWPTLPRHNLTAVSQVQEQLOCKHNL 390
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 360 PPWMDWFHGGLOFQIEHHLFPKMPRCNLRKISPYVIELCKHNL 405

```

```

RESULT 7
US-08-834-655-7
; Sequence 7, Application US/08834655
; Patent No. 5968809
; GENERAL INFORMATION:
; APPLICANT: KNUTZON, DEBORAH

```

TELEFAX: (650) 328-4477
 TELETYPE: N/A
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 355 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-834-655-5

Query Match 24.7%; Score 565; DB 2; Length 355;
 Best Local Similarity 34.9%; Pred. No. 1.3e-58;
 Matches 127; Conservative 58; Mismatches 145; Indels 34; Gaps 6;

QY 82 DFRKRLREELIATGMDASPLWYSKISTITGLGLVGLVLMVQYOM-----YFIGAVLLGM 136
 DB 1 EVKRLTLFOSLGYDSSKAYAFKVSFNLICINGLSTVIIVAKWGQTSTLANVLNLSAALLGL 60
 QY 137 HYQOMGWLSDICHQHFKNRNNNVLGLVFGNGLOGFSVTCWKDRHNAHHSATNVQGH 196
 DB 61 FWOCCGWLADFLHQVQDFRFGDLFGALGGVQCQFSSSSWKKDHTHHAAPNVHGED 120
 QY 197 PDIDNLPPLAWSDDVTRASPI-----SRKLIQFOQYIFLVICILLRIFWCQCVL 247
 DB 121 PDIDTHTPLTWSHALEMFSDVPDELTRMWSREMLNQTWTFPPILSFARLSWCLQSIL 180
 QY 248 TVSLKDRDQNFQYRSQYKK-----EAIGLALHWTALKALFLHFLFMPSLTSLVFFVSEL 301
 DB 181 FVLPL-----NGCAHKSGARVPSISLEQLSLAMHWTYLAFTNLFKDPVNNMLVFLVSQA 236
 QY 302 VGGFGIAIVFMNHYPLEKIGDPVMDGHSVGOIHETMNRIRGIIIDWFEGGLNYQIEH 361
 DB 237 VCNLLAIVFSLNHNHNPVTSKEAVDMDFTKIIITGRDVHPGLFANWFTGGLNYQIEH 296
 QY 362 HLMPITLPHNLTAIVSYQVQLCQKHNLPYRNPPLPHEGLVILLRLVLAFAEAKQPA--- 419
 DB 297 HLEPSPMRHNFESKIQPAVETLCKKYNRYHTTGMEGTA-----EVFSRLNEYSKAASK 350
 QY 419 -GKA 421
 DB 351 MGKA 354

RESULT 4
 US-08-366-779-5
 Sequence 5, Application US/08366779
 Patent No. 5614393
 GENERAL INFORMATION:
 APPLICANT: Thomas, Terry L.
 APPLICANT: Reddy, Avutu S.
 APPLICANT: Nuccio, Michael
 APPLICANT: Freyssinet, Georges L.
 APPLICANT: Numburg, Andrew N.
 TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
 TITLE OF INVENTION: DELTA 6-DESATURASE
 NUMBER OF SEQUENCES: 25
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Scully, Scott, Murphy & Presser
 STREET: 400 Garden City Plaza
 CITY: Garden City
 STATE: New York
 COUNTRY: United States
 ZIP: 11530
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/366,779
 FILING DATE: 30-DEC-1994

CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: Presser, Leopold
 REGISTRATION NUMBER: 19,827
 REFERENCE/DOCKET NUMBER: 8383ZYXW
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (516) 742-4343
 TELEFAX: (516) 742-4366
 TELEX: 230 901 SANS UR
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 448 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-366-779-5

Query Match 19.0%; Score 433.5; DB 1; Length 448;
 Best Local Similarity 29.8%; Pred. No. 7.6e-43;
 Matches 121; Conservative 67; Mismatches 167; Indels 51; Gaps 14;

QY 11 LQLMQOTYDYSAWNPHPGGAEIIEYQGRDATDAFVMVHFQEAFLKRMKPINPSPEL 70
 DB 25 ISIQKAYDSDWKDHPGGSFPLKSLAGQEVTDFAVAFHASTW---KNLDKFTTGYL 81
 QY 71 PPOAAVNEAEDFKRLREELIATGMDA-----SPLWYSYKISTITGLGLVGLVLMVQY 124
 DB 82 -KDYSVSEVSKDYAKLVFEFSKMGLYDKGHIMEPATLCF---IAMLFAMSYGVLFCEGV 137
 QY 125 QMFIAGVALLGMHQMGWLSHDICHQTFKNRNNNVLGLVFGNGLOGFSVTCWKDRHN 184
 DB 138 LVHLSFCGLMFLWISQWIGHAGHYMVVSDSLNFMFGIFAANCUSGISGIGWKNHN 197
 QY 185 AHSATNVQGHDPIDNLPPLAWS-----EDDVTRASPIRKRKLIQFOQYFLV 232
 DB 198 AHTACSLSEYDPLQIPLVYSSKFFGSLTSHFEKRLTFDS-LSRFFVSYQHWTFP 256
 QY 233 ICILLRIFWCQCVLTVRSKDRDNQYRSQYKKEATGLAHWTALKALFLHFLFHPSPILTS 292
 DB 257 IMCAARLNMVQSLI---MLLTNRNVSRAQ---ELLGC-----LVFSIWY--PLVLS 301
 QY 293 LL-----VFFVSELVGGFGIAIVF--MNHVPLE-KIGDPVMDGHSVGOIHETMNR 344
 DB 302 CLPNWGERIMFVIASLSVTGMQVQVQFSLNHFSSSVYVCKP--KGNWFKEKOTDGLDISC 359
 QY 345 GIITDWFEGGLNYQIEHLMPTLPHNLTAIVSYQVQLCQKHNLPY 390
 DB 360 PPWMDWPHGGSQFOIEHHLFPKMPRCNLRKISPYVIELCKKHNLPY 405

RESULT 5
 US-08-789-936-5
 Sequence 5, Application US/08789936
 Patent No. 5782220
 GENERAL INFORMATION:
 APPLICANT: Thomas, Terry L.
 APPLICANT: Reddy, Avutu S.
 APPLICANT: Nuccio, Michael
 APPLICANT: Freyssinet, Georges L.
 APPLICANT: Numburg, Andrew N.
 TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
 TITLE OF INVENTION: DELTA 6-DESATURASE
 NUMBER OF SEQUENCES: 25
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Scully, Scott, Murphy & Presser
 STREET: 400 Garden City Plaza
 CITY: Garden City
 STATE: New York
 COUNTRY: United States
 ZIP: 11530
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk

Db 81 -----ANFYV---GDIDESDRDIKNDFAAEVRKRLTLFQSLGYDSSKAYAFKVSFN 131
Qy 111 LGLGVLGYFLMAYQYOM-----YFICAVLLGMHYQOMGLSHDICHQHTQFKNNWNLVGL 165
Db 132 LCINGLSVIVAKWGQSTLANVLSAALLGLFWQCGGLAHDFLHHQVFDQDFWGLDGLFGA 191
Qy 166 VFGNLOGFSVTCWKDRHNAHSATNVQGHDPDIDNLPPLAWSDDVTRASPI-----219
Db 192 FLGGVCGQFSSSWKDKHNTHAAPNVHGEDPDIDTHTLWSEHALENFSDVPDEELTR 251
Qy 219 --SRKLIQFOQYFLVICILLRFIWCFCVLTVRSLKDRDNQFYRSQYKK-----EAG 270
Db 252 MWSRFMVLNQTWFYFPIILSWCLQSILFVLP-----NGQAHKPSGARVPISLVEQLS 307
Qy 271 LALHWTALKALHFLFMPISILSLVFFVSELVGGFIAIVFMNHYPLEKIGDPVWDG 330
Db 308 LAMHWTWYLAFTMFLFKDPVNMVLYFLVSOAVCGNLLAIVFSLNHNMPVSKESAEVDM 367
Qy 331 FSVQIHTMNRIRGIITDWFEGGLNYQIEHHLWPTLPRHNLTAVSQVEOLCKHNL 390
Db 368 FTFQIITGRDVHPLGFANWFTGGLNYQIEHHLFSPMRHNFSKIOPAVETLCKKYNRY 427
Qy 391 RNPLPHEGLVILLRYLAVFARMAEKQPA-----GKA 421
Db 428 HTTGMIETGA-----EVFSRLNEVSKAASKMGKA 456

RESULT 2

US-08-833-610-4
; Sequence 4, Application US/08833610
; Patent No. 5972664
; GENERAL INFORMATION:
; APPLICANT: KNUZON, DEBORAH
; APPLICANT: MURKERJI, PRADIP
; APPLICANT: HUANG, YUNG-SHENG
; APPLICANT: THURMOND, JENNIFER
; APPLICANT: CHAUDHARY, SUNITA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
; OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
; STREET: 260 SHERIDAN AVE, P.O. BOX 60039
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833,610
; FILING DATE: 11-APR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: RAE-VENTER, BARBARA
; REGISTRATION NUMBER: 32,750
; REFERENCE/DOCKET NUMBER: CGNE.123.000S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)328-4400
; TELEFAX: (650)328-4477
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 457 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-833-610-4

Query Match 27.28; Score 622; DB 2; Length 457;
Best Local Similarity 32.78; Pred. No. 3.3e-65;
Matches 149; Conservative 76; Mismatches 174; Indels 56; Gaps 11;

Qy 2 KSKROALSPLOLM--EQYDVSAWVNFPHPGGAIEITENQGRDATDAFVMVHFOEAFDKLK 59
Db 23 EGKDAEAPFLMIDNKYVDYREFVPDHPGGS-VLLTHVGKDGTDVDFTHPEAAWETL- 81
Qy 60 RMPKINPSELPPOAAVNEAQEDF-----RKLREELIATGMFEDASPLWYSYKISTT 110
Db 81 -----ANFYV---GDIDESDRDIKNDFAAEVRKRLTLFQSLGYDSSKAYAFKVSFN 131
Qy 111 LGLGVLGYFLMAYQYOM-----YFICAVLLGMHYQOMGLSHDICHQHTQFKNNWNLVGL 165
Db 132 LCINGLSVIVAKWGQSTLANVLSAALLGLFWQCGGLAHDFLHHQVFDQDFWGLDGLFGA 191
Qy 166 VFGNLOGFSVTCWKDRHNAHSATNVQGHDPDIDNLPPLAWSDDVTRASPI-----219
Db 192 FLGGVCGQFSSSWKDKHNTHAAPNVHVEDPDIDTHTLWSEHALENFSDVPDEELTR 251
Qy 219 --SRKLIQFOQYFLVICILLRFIWCFCVLTVRSLKDRDNQFYRSQYKK-----EAG 270
Db 252 MWSRFMVLNQTWFYFPIILSWCLQSILFVLP-----NGQAHKPSGARVPISLVEQLS 307
Qy 271 LALHWTALKALHFLFMPISILSLVFFVSELVGGFIAIVFMNHYPLEKIGDPVWDG 330
Db 308 LAMHWTWYLAFTMFLFKDPVNMVLYFLVSOAVCGNLLAIVFSLNHNMPVSKESAEVDM 367
Qy 331 FSVQIHTMNRIRGIITDWFEGGLNYQIEHHLWPTLPRHNLTAVSQVEOLCKHNL 390
Db 368 FTFQIITGRDVHPLGFANWFTGGLNYQIEHHLFSPMRHNFSKIOPAVETLCKKYNRY 427
Qy 391 RNPLPHEGLVILLRYLAVFARMAEKQPA-----GKA 421
Db 428 HTTGMIETGA-----EVFSRLNEVSKAASKMGKA 456

RESULT 3

US-08-834-655-5
; Sequence 5, Application US/08834655
; Patent No. 5968809
; GENERAL INFORMATION:
; APPLICANT: KNUZON, DEBORAH
; APPLICANT: MURKERJI, PRADIP
; APPLICANT: HUANG, YUNG-SHENG
; APPLICANT: THURMOND, JENNIFER
; APPLICANT: CHAUDHARY, SUNITA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
; OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
; STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,655
; FILING DATE: 11-APR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: RAE-VENTER, BARBARA
; REGISTRATION NUMBER: 32,750
; REFERENCE/DOCKET NUMBER: CGNE.124.000S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 328-4400

QY 298 VSELVGGFGIAIVFNNHYPLEKIGDPVMDGHGFSVQIHTMNIIRRGITDWFEGGLNY 357
 DB 175 FIRELESHFWVWVQNMHIVMEIDQAYRD--WFS-SQLTATCNVQSFDFWFSGLNLF 231
 QY 358 QIEHHLWPTLPRNLTAVSYQVEQLCKOKNLPYRNPLPHEGLVILLRYL 406
 DB 232 QIEHHLFPTMPRNHLKIAPLVKSLCAKHGIEYQERKPLLRALLDIIRSL 280

RESULT 14
 W95513
 ID W95513 standard; Protein: 615 AA.
 AC W95513;
 DT 26-MAR-1999 (first entry)
 DE Amino acid sequence of human desaturase gene contig 2535.
 KW Delta 5 desaturase; recombinant; fatty acid desaturase; FAD; PUFA; oil;
 KW polyunsaturated fatty acid; linoleic acid; arachidonic acid; linolenic;
 KW stearidonic acid; eicosapentaenoic acid; malnutrition; feeding formula;
 KW dietary supplement; prostaglandin; restenosis; angioplasty; inflammation;
 KW rheumatoid arthritis; psoriasis; osteoporosis; cancer; eczema; AIDS;
 KW diabetes; cosmetic; animal feed; human.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Misc_difference 295 /note= "encoded by TGA"
 FT Misc_difference 321 /note= "encoded by TGA"
 FT Misc_difference 458 /note= "encoded by TGA"
 FT Misc_difference 491 /note= "encoded by TAA"
 FT Misc_difference 517 /note= "encoded by TAG"
 FT Misc_difference 535 /note= "encoded by TGA"
 FT Misc_difference 550 /note= "encoded by TGA"
 FT Misc_difference 615 /note= "encoded by TG"
 PN W09846764-A1.
 PD 22-OCT-1998.
 PE 10-APR-1998; U07421.
 PR 24-OCT-1997; US-956985.
 PR 11-APR-1997; US-833610.
 PR 11-APR-1997; US-834033.
 PR 11-APR-1997; US-834655.
 PA (ABBO) ABBOTT LAB.
 PA (CALJ) CALGENE LLC.
 PI Chaudhary S, Huang Y, Knutzon D, Leonard AE, Mukerji P,
 PI Thurmond J;
 DR WPI: 99-080739/07.
 DR N-PSDB: X00909.
 PT Nucleic acid construct able to express fatty acid desaturase in
 PT plants - useful in human or animal nutrition, as cosmetics and
 PT therapeutically, e.g. for restenosis, cancer and diabetes
 PS Claim 48; Page 167-169; 210pp; English.
 CC The invention relates to a nucleic acid construct that contains at least
 CC one of the nucleotide sequences (X00899 to X00891) encoding Mortierella
 CC alpina delta 6, delta 12 and delta 5 desaturases (W95504 to W95506)
 CC respectively, coupled to an expression control sequence functional in
 CC plants. Recombinant plant cells containing at least one DNA encoding a
 CC M. alpina fatty acid desaturase (FAD), can be used for the production of
 CC polyunsaturated fatty acid (PUFA). These recombinant cells or plants
 CC containing them are used to produce oils such as linoleic acid,
 CC arachidonic acid, gamma-linolenic acid, dihomo-gamma-linolenic acid,
 CC stearidonic acid and eicosapentaenoic acid (EPA). These plant oils are
 CC used: (i) to treat malnutrition; (ii) in infant feeding formulas, or
 CC dietary supplements or substitutes, for use in humans or animals; (iii)
 CC for treating disorders associated with inadequate consumption or
 CC production of PUFA (or their metabolites such as prostaglandins), e.g.
 CC restenosis after angioplasty, inflammation, AIDS, rheumatoid arthritis,
 CC psoriasis, osteoporosis, cancer, eczema, diabetes; (iv) as cosmetics, and

CC (v) as animal feeds. Fragments of the DNA are used as probes to isolate
 CC related coding sequences. Recombinant plants can produce high yields of
 CC PUFA, since new pathways can be created and unwanted ones suppressed.
 CC Plants can be engineered to express oils of particular PUFA composition,
 CC e.g. one similar to that in human milk, and product recovery is simpler
 CC than with e.g. fish. Sequences W95508-514 represent amino acid sequences
 CC of various contigs of human desaturase genes which are similar to the
 CC M. alpina desaturase sequences.
 SQ Sequence 615 AA;

Query Match 13.6%; Score 310; DB 1; Length 615;
 Best Local Similarity 29.4%; Pred No. 1.1e-27;
 Matches 85; Conservative 46; Mismatches 126; Indels 32; Gaps 8;
 QY 129 IGAVLGMHYQQMGWLSHDICHHQTFTKNNMNNLVGLFNGLOGFSVTCWKDRHNAHS 189
 DB 13 ITAFVLATSOAQAGWLOHDYGVHLSVYRKPKWNHVKFVIGHLKGASANNWNRHFQHA 72
 QY 189 ATNVOGHDDIDMLPLPANEEDVTRSPIT--SRKLIQF-----QQYYFLV-ICILLRF 239
 DB 73 KPNIFHKDPDVMNMLHVFVLGE-----WQPIEYGGKKLKLPLYNHQHEYFFLGGPLLP 127
 QY 240 IMCFQCVLTVRSLSKDRDNQFYRSQYKKEAIGLALHWTALRFLHFFMP--SILTSLVFF 297
 DB 128 YFOIILMTM-----IVHKNWVDLAWAVSYIRFTYIPFYGILGALLFLN 174
 QY 298 VSELVGGFGIAIVFNNHYPLEKIGDPVMDGHGFSVQIHTMNIIRRGITDWFEGGLNY 357
 DB 175 FIRELESHFWVWVQNMHIVMEIDQAYRD--WFS-SQLTATCNVQSFDFWFSGLNLF 231
 QY 358 QIEHHLWPTLPRNLTAVSYQVEQLCKOKNLPYRNPLPHEGLVILLRYL 406
 DB 232 QIEHHLFPTMPRNHLKIAPLVKSLCAKHGIEYQERKPLLRALLDIIRSL 280

RESULT 15
 W84141
 ID W84141 standard; Peptide: 252 AA.
 AC W84141;
 DT 15-FEB-1999 (first entry)
 DE Desaturase enzyme peptide sequence.
 KW Fatty acid; desaturase; polyunsaturated fatty acid;
 KW malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis;
 KW cancer; diabetes; eczema; platelet aggregation; vasodilation;
 KW cholesterol level; endometriosis; premenstrual syndrome;
 KW myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;
 KW acute respiratory syndrome; hypertension; inflammatory skin disorder.
 OS Unidentified.
 PN W09846763-A1.
 PD 22-OCT-1998.
 PE 10-APR-1998; U07126.
 PR 11-APR-1997; US-834655.
 PA (ABBO) ABBOTT LAB.
 PA (CALJ) CALGENE LLC.
 PI Chaudhary S, Huang Y, Knutzon D, Leonard AE, Mukerji P,
 PI Thurmond J;
 DR WPI: 98-594582/50.
 PT New isolated fatty acid desaturase enzymes - used for the production
 PT of polyunsaturated fatty acids for use in, e.g. pharmaceutical
 PT compositions, nutritional compositions, cosmetics or animal feed
 PS Example 2; Pages 103-104; 165pp; English.
 CC The present sequence represents a peptide derived from a desaturase
 CC enzyme. The specification describes methods for desaturating a
 CC fatty acid and for producing a desaturated fatty acid by expressing
 CC increased levels of a desaturase. Desaturases can be used for
 CC desaturating fatty acids. The enzymes can be used to produce
 CC polyunsaturated fatty acids, which can be used for treating malnutrition,
 CC in pharmaceutical compositions, in cosmetics or in animal feed. The
 CC polyunsaturated fatty acids can be used for treating e.g. restenosis
 CC after angioplasty, inflammation, rheumatoid arthritis, asthma, psoriasis,
 CC cancer, diabetes or eczema or reduce blood pressure. They can also be
 CC used to inhibit platelet aggregation, cause vasodilation, lower

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Db 416 RSL 418

RESULT 12
ID W84155
AC W84155;
DE Human desaturase enzyme encoded by contig 2535.
KW Fatty acid; desaturase; polyunsaturated fatty acid;
KW malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis;
KW cancer; diabetes; eczema; platelet aggregation; vasodilation;
KW cholesterol level; endometriosis; premenstrual syndrome; human;
KW myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;
KW acute respiratory syndrome; hypertension; inflammatory skin disorder.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Misc_difference 608 /note= "not specified"
FT PN W09846763-A1.
FD 22-OCT-1998.
PF 10-APR-1998; U07126.
PR 11-APR-1997; US-834655.
PA (ABBO ) ABBOTT LAB.
PA (CALJ ) CALGENE LLC.
PI Chaudhary S, Huang Y, Knutzon D, Leonard AE, Mukerji P,
PI Thurmond J;
DR WPI; 98-594582/50.
DR N-PSDB; V63642.
PT New isolated fatty acid desaturase enzymes - used for the production
PT of polyunsaturated fatty acids for use in, e.g. pharmaceutical
PT compositions, nutritional compositions, cosmetics or animal feed
PT Example 12; Pages 123-124; 163pp; English.
CC The present sequence is a human desaturase enzyme. The cDNA sequence was
CC identified based on homology between human cDNA sequences and Mortierella
CC alpina desaturase gene sequences. The specification describes methods for
CC desaturating a fatty acid and for producing a desaturated fatty acid by
CC expressing increased levels of a desaturase. The enzyme can be used for
CC desaturating fatty acids. The enzyme can be used to produce
CC polyunsaturated fatty acids, which can be used for treating malnutrition,
CC in pharmaceutical compositions, in cosmetics or in animal feed. The
CC polyunsaturated fatty acids can be used for treating e.g. restenosis
CC after angioplasty, inflammation, rheumatoid arthritis, asthma,
CC psoriasis, cancer, diabetes or eczema or reduce blood pressure. They
CC can also be used to inhibit platelet aggregation, cause vasodilation,
CC lower cholesterol levels, inhibit proliferation of vessel wall smooth
CC muscle and fibrous tissue, reduce or prevent gastro-intestinal bleeding
CC and other side effects caused by non-steroidal anti-inflammatory drugs,
CC prevent or treat endometriosis and premenstrual syndrome, treat myalgic
CC encephalomyelitis and chronic fatigue after viral infections, treat
CC AIDS, multiple sclerosis, acute respiratory syndrome, hypertension and
CC inflammatory skin disorders.
SQ Sequence 608 AA;

Query Match 13.6%; Score 310; DB 1; Length 608;
Best Local Similarity 29.4%; Pred. No. 1.1e-27;
Matches 8; Conservative 46; Mismatches 126; Indels 32; Gaps 8;

QY 129 IGAVLLGMHYQOMGWLSDICHQHTFKNRNNNLVGLVFGNGLOGFSVTCWKDRHNAHNS 188
DB 13 ITAFVLATSAQAQAGWLQHDYGLSVYRKPKNHLVHKVIGHLKGASANNWNRHFQHA 72

QY 189 ATNVQGHDPDNDLNPPLAWSEDDVTRASPI--SRKLQF-----QQYFLV-ICILLRF 239
DB 73 KPNFHKDPDNDVNLHVFVLGE-----WQPIEYGGKKLKLPLYNHGHQHYFFLIGPLPLIPM 127

QY 240 IWCFQCVLTVRSLKDRDNQFYSQYKKEAIGLALHTLWTLKALFLHFFMP--SILTSLLVFF 297
DB 128 YFQIQIITM-----IVHKNWDLANAVSYIIRFFITYIPFYIGLIGALLFLN 174

QY 298 VSELVGGFGIAIVFMNHPLEKIGDPVMDGHSVGVQIHETMNRRIITDWFEGGLNY 357
DB 128 YFQIQIITM-----IVHKNWDLANAVSYIIRFFITYIPFYIGLIGALLFLN 174

Db 175 FIRELESHWFVWVTQMNHYMEIQEAYRD--WFS-SOLTATCNVEQSFNDWFSGLNLF 231

QY 358 QIEHHLNPTLPRHNLTAVSQVEQLCKQKHNLPRNPLPHEGLVILLRYL 406
DB 232 QIEHHLFPTMPRHNLHKLAPLVKSLCAKKGIEYQEKPLRLALLDIRSL 280

RESULT 13
ID W85134
AC W85134;
DE A desaturase enzyme encoded by contig 2535.
KW Fatty acid; desaturase; polyunsaturated fatty acid;
KW malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis;
KW cancer; diabetes; eczema; platelet aggregation; vasodilation;
KW cholesterol level; endometriosis; premenstrual syndrome;
KW myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;
KW acute respiratory syndrome; hypertension; inflammatory skin disorder.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Misc_difference 608 /note= "not specified"
FT PN W09846765-A1.
FD 22-OCT-1998.
PF 10-APR-1998; U07422.
PR 11-APR-1997; US-833610.
PA (ABBO ) ABBOTT LAB.
PA (CALJ ) CALGENE LLC.
PI Chaudhary S, Huang Y, Knutzon D, Leonard AE, Mukerji P,
PI Thurmond J;
DR WPI; 99-009334/01.
DR N-PSDB; V82641.
PT New nucleic acid encoding delta5 and other desaturase enzymes -
PT useful in production of oils of increased arachidonic acid content,
PT used, e.g. for treating cancer, as foods, animal feeds and cosmetics
PT Claim 87; Pages 117-119; 153pp; English.
CC The present sequence represents a human desaturase enzyme. The enzyme
CC sequence is used in the methods of the invention. The specification
CC describes methods for desaturating a fatty acid and for producing a
CC desaturated fatty acid by expressing increased levels of a desaturase.
CC The enzyme can be used for desaturating fatty acids. The enzyme can be
CC used to produce polyunsaturated fatty acids, which can be used for
CC treating malnutrition, in pharmaceutical compositions, in cosmetics or
CC in animal feed. The polyunsaturated fatty acids can be used for treating
CC e.g. restenosis after angioplasty, inflammation, rheumatoid arthritis,
CC asthma, psoriasis, cancer, diabetes or eczema or reduce blood pressure.
CC They can also be used to inhibit platelet aggregation, cause
CC vasodilation, lower cholesterol levels, inhibit proliferation of vessel
CC wall smooth muscle and fibrous tissue, reduce or prevent
CC gastro-intestinal bleeding and other side effects caused by non-steroidal
CC anti-inflammatory drugs, prevent or treat endometriosis and premenstrual
CC syndrome, treat myalgic encephalomyelitis and chronic fatigue after
CC viral infections, treat AIDS, multiple sclerosis, acute respiratory
CC syndrome, hypertension and inflammatory skin disorders.
SQ Sequence 608 AA;

Query Match 13.6%; Score 310; DB 1; Length 608;
Best Local Similarity 29.4%; Pred. No. 1.1e-27;
Matches 8; Conservative 46; Mismatches 126; Indels 32; Gaps 8;

QY 129 IGAVLLGMHYQOMGWLSDICHQHTFKNRNNNLVGLVFGNGLOGFSVTCWKDRHNAHNS 188
DB 13 ITAFVLATSAQAQAGWLQHDYGLSVYRKPKNHLVHKVIGHLKGASANNWNRHFQHA 72

QY 189 ATNVQGHDPDNDLNPPLAWSEDDVTRASPI--SRKLQF-----QQYFLV-ICILLRF 239
DB 73 KPNFHKDPDNDVNLHVFVLGE-----WQPIEYGGKKLKLPLYNHGHQHYFFLIGPLPLIPM 127

QY 240 IWCFQCVLTVRSLKDRDNQFYSQYKKEAIGLALHTLWTLKALFLHFFMP--SILTSLLVFF 297
DB 128 YFQIQIITM-----IVHKNWDLANAVSYIIRFFITYIPFYIGLIGALLFLN 174

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Query Match	18.5%	Score 421.5;	DB 1;	Length 746;
Best Local Similarity	28.1%	Pred. No. 1e-40;		
Matches 119;	Conservative	72;	Mismatches 177;	Indels 55; Gaps 13;

QY	11	LQLMEQTYDVSANVNFHFGAGIEITENYQGRDATAFVWVHHFOEAFDK-----LKRMPK	63
		: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	
DB	24	LVTDRKYNISEFTRRHPGGSRVISHYAGODATDPFAFHINKGLVKKXNNLSLIGELSP	83
		: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	
QY	64	INPSFELPPQAAVNEAOEDFRKLREELIATGMFASPLWYSYKI-----STTLGLGV	115
		: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	
DB	84	EQPSFE--PTKNELTDFEFLRATVERMGLMKANHVFFLLYLHLLLDGAAWLTWV	140
		: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	
QY	116	LGVFLMVQYQMYFICAGVLLGHNYQ-QMGWLSHDICHHOTFKNRNNNNLVGLVFGNGLQGF	174
		: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	
DB	141	FG----TSFLPFLCAVILSAVQQAQAGWLQHDYGHLSVYRKRPKNHVLVHKFVIGHLKGA	196
		: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	
QY	175	SVTCWKDRHNAHHSATNVQGHDPIDNLPPLAWSDDVTRASPI--SKRLIQF-----Q	226
		: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	
DB	197	SANWNNRHFFQHHAKPIFHKDPDVMHLEVFLGE-----WQPIEYGGKKLKYLPYNHQH	251
		: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	
QY	227	QYVFLV-ICILLRFIWCFOCVLTVRSCLKDRNQFVRSQYKKEAGIALHLHWLKALFHLFF	285
		: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	
DB	252	EYFLGPGPLIPMYFQYIITMW-----IVHKNWVDLAWAVSYIRFFITY	298
		: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	
QY	286	MP--SILTSLLVFVSELVGGFIAVFMNHHYPLEKIGDPVMDGHGFSVGQIHETMNIR	343
		: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	
DB	299	IPYGIIGALLFLNFIRFLESHWFVWYTMNHHVMEIDQEAIRD-WFS-SQLTATCNVE	355
		: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	
QY	344	RGIITDMFFGGLNQVIEHHLWPTLPRHNLTAVSQVEQLCOKHNLPLRNPPLPHEGLVILL	403
		: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	
DB	356	QSEFNDWFSGLNFQIEHHLFPTMPRHNLHRIAPLVKSLCAKHGIEYQEKPLLRALLDII	415
		: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	
QY	404	RYL	406
		: : : :	
DB	416	RSI	418
		: : : :	

RESULT	11
W95514	
ID	W95514 standard; Protein; 753 AA.
AC	W95514;
DE	26-MAR-1999 (first entry)
DE	Amino acid sequence of human desaturase gene contig 25338a.
KW	Delta 5 desaturase; recombinant; fatty acid desaturase; FAD; PUFA; oil;
KW	polyunsaturated fatty acid; linoleic acid; arachidonic acid; linolenic;
KW	stearidonic acid; eicosapentaenoic acid; malnutrition; feeding formula;
KW	dietary supplement; prostaglandin; restenosis; angioplasty; inflammation;
KW	rheumatoid arthritis; psoriasis; osteoporosis; cancer; eczema; AIDS;
KW	diabetes; cosmetic; animal feed; human.
OS	Homo sapiens.
FN	Key
FT	Location/Qualifiers
FT	Misc_difference 433 /note= "encoded by TGA"
FT	FT
FT	Misc_difference 459 /note= "encoded by TGA"
FT	FT
FT	Misc_difference 596 /note= "encoded by TGA"
FT	FT
FT	Misc_difference 629 /note= "encoded by TAA"
FT	FT
FT	Misc_difference 655 /note= "encoded by TAG"
FT	FT
FT	Misc_difference 673 /note= "encoded by TGA"
FT	FT
FT	Misc_difference 688 /note= "encoded by TGA"
FT	FT
FT	Misc_difference 753 /note= "encoded by TG"
FT	FT
PN	W09846764-A1.
PD	22-OCT-1998.
PF	10-APR-1998; U07421.
PR	24-OCT-1997; US-956985.
PR	11-APR-1997; US-833610.
PR	

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PR 11-1997; US-834033.
PR 11-APR-1997; US-834655.
PA (ABBO ) ABBOTT LAB.
PA (CALJ ) CALGENE LLC.
PI Chaudhary S, Huang Y, Knutzon D, Leonard AE, Mukerji P,
PI Thurmond J.
DR WPI; 99-080739/07.
DR N-PSDB; X00910.
DR Nucleic acid construct able to express fatty acid desaturase in
PT plants - useful in human or animal nutrition, as cosmetics and
PT therapeutically, e.g. for restenosis, cancer and diabetes
PS Claim 48: Page 169-171: 210pp; English.
CC The invention relates to a nucleic acid construct that contains at least
CC one of the nucleotide sequences (X00889 to X00891) encoding Mortierella
CC alpina delta 6, delta 12 and delta 5 desaturases (W93504 to W93506)
CC respectively, coupled to an expression control sequence functional in
CC plants. Recombinant plant cells containing at least one DNA encoding a
CC M. alpina fatty acid desaturase (FAD), can be used for the production of
CC polyunsaturated fatty acid (PUFA). These recombinant cells or plants
CC containing them are used to produce oils such as linoleic acid,
CC arachidonic acid, gamma-linolenic acid, dihomogamma-linolenic acid,
CC stearidonic acid and eicosapentaenoic acid (EPA). These plant oils are
CC used: (i) to treat malnutrition; (ii) in infant feeding formulas, or
CC dietary supplements or substitutes, for use in humans or animals; (iii)
CC for treating disorders associated with inadequate consumption or
CC production of PUFA (or their metabolites such as prostaglandins), e.g.
CC restenosis after angioplasty, inflammation, AIDS, rheumatoid arthritis,
CC psoriasis, osteoporosis, cancer, eczema, diabetes; (iv) as cosmetics, and
CC (v) as animal feeds. Fragments of the DNA are used as probes to isolate
CC related coding sequences. Recombinant plants can produce high yields of
CC PUFA, since new pathways can be created and unwanted ones suppressed.
CC Plants can be engineered to express oils of particular PUFA composition,
CC e.g. one similar to that in human milk, and product recovery is simpler
CC than with e.g. fish. Sequences W95508-514 represent amino acid sequences
CC of various contigs of human desaturase genes which are similar to the
CC M. alpina desaturase sequences.
CC Sequence 753 AA;
SQ

Query Match 18.5% Score 421.5; DB 1; Length 753;
Best Local Similarity 28.1%; Pred. No. 1.1e-40;
Matches 119; Conservative 72; Mismatches 177; Indels 55; Gaps 13

QY 11 LQMLEQYDYSAWNFHPGGAEIENYQGRDATDAFMVWHFOEAPDK-----LKRMPK 63
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
D6 LVDRKYVNISEFRRHPGGSRVISHVAGQADTPFVAFHINKGLVKRYMNSLLIGELSP 83
QY 64 INPSFELPPQANVNEAQEDFKRLREELIATGMFASPLWSYKI-----STTLGLGV 115
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
D6 EOPSFE---PTKNKELTDEFRELATYERMGLMKANHVFFLLYLHLILLDGAAWLTLMV 140
QY 116 LGYELMWQYQMYFGVILGMHYQ-QMGVLSHDICHQTFKNRNWNVLVLGVFGNGLOGF 174
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
D6 141 FG----TSFPLFLCALVLLSVQAQAGWLQHDYGLHSYRKPKWNHLVHFVIGHLKA 196
QY 175 SVTCWKDRHNAHSATNVQGHDPIDNLPPLAWSDEDDYTRASPI--SRKLQF-----Q 226
DB 197 SANWNHRHFQGHAKPNIFHKDPDVMNLHVPVLGE----WQPIEYKKKKLYLPYNHOH 251
QY 227 QYXELV-ICILIRIFWFCQVLTVRSUKDRDNQYRSQYKKEATGLAHWTLKALFLHFF 285
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
D6 252 EYFFLIGPLLPIMFYQYQIITM-----IVHKNWVDLAWAVSYIRFFITY 298
QY 286 MP--SILTSLVFFVSELVGGFGTAIVFNMNHYPLEKIDGPVWDGHHGFSVGOIHETMNR 343
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
D6 299 IPFYIGALLFLNFIIRFLSHWVFWVTQMNNHVIWEIDQEAYRD--WFS-SOLTATCNVE 355
QY 344 RGIITDFFGGLNYQIEHHLWPTLPRNHLTAVSVQVEOLCQKHNLPLYRNPFLPHEGLVILL 403
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
D6 356 QSFNDWFSGHLNFQIEHHLFPTPRNHLNHLIAPIVKSCLKAHGIEYQEKPLLRALLDII 415
QY 404 RYL 406
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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RESULT	ID	W95514	standard; Protein; 753 AA.
11	AC	W95514;	
	DT	26-MAR-1999	(first entry)
	DE	Amino acid sequence of human desaturase gene contig 253538a.	
	KW	Delta 5 desaturase; recombinant; fatty acid desaturase; FAD; PUFA; oil;	
	KW	polyunsaturated fatty acid; linoleic acid; arachidonic acid; linolenic;	
	KW	stearidonic acid; eicosapentaenoic acid; malnutrition; feeding formula;	
	KW	dietary supplement; prostaglandin; restenosis; angioplasty; inflammation;	
	KW	rheumatoid arthritis; psoriasis; osteoporosis; cancer; eczema; AIDS;	
	KW	diabetes; cosmetic; animal feed; human.	
	OS	Homo sapiens.	
	FS	Homo sapiens.	
	Key	Location/Qualifiers	
	FT	Misc_difference 433	/note= "encoded by TGA"
	FT	Misc_difference 459	/note= "encoded by TGA"
	FT	Misc_difference 596	/note= "encoded by TGA"
	FT	Misc_difference 629	/note= "encoded by TGA"
	FT	Misc_difference 655	/note= "encoded by TAA"
	FT	Misc_difference 673	/note= "encoded by TAG"
	FT	Misc_difference 688	/note= "encoded by TGA"
	FT	Misc_difference 753	/note= "encoded by TGA"
	FT	Misc_difference 753	/note= "encoded by TG"
	PN	WO9846764-A1.	
	PD	22-OCT-1998.	
	PF	10-APR-1998;	U07421.
	PR	24-OCT-1997;	US-956985.
	PR	11-APR-1997;	US-833610.

Db 302 CLPNWGERIMFVIAISLVTGQQVQFSLNHFFSSVYVVKP--KGNWFEKOTDGTDLDISC 359

QY 345 GIITDFFGGLNQIEHLLPTLPRNLTAVSQVQEOQLCKHNLPLY 390

Db 360 PFWDMFHHGLQFQIEHLLFPKPRCNLRKISPYVIELCKHNLPLY 405

RESULT 9

W84156

ID W84156 standard; Protein: 746 AA.

AC W84156; (first entry)

DE Human desaturase enzyme encoded by contig 253538a.

KW Fatty acid; desaturase; polyunsaturated fatty acid;

KW malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis;

KW cancer; diabetes; eczema; platelet aggregation; vasodilation;

KW cholesterol level; endometriosis; premenstrual syndrome; human;

KW myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;

KW acute respiratory syndrome; hypertension; inflammatory skin disorder.

OS Homo sapiens.

EH Key

FT Misc_difference 746

FT /note= "not specified"

PN W09846763-A1.

PD 22-OCT-1998.

PF 10-APR-1998: U07126.

PR 11-APR-1997: US-834655.

PA (ABBO) ABBOTT LAB.

PA (CALJ) CALGENE LLC.

PI Chaudhary S, Huang Y, Knutzon D, Leonard AE, Mukerji P,

PI Thurmond J;

DR WPI: 98-594582/50.

DR N-PSDB: V63643.

PT New isolated fatty acid desaturase enzymes - used for the production

PT of polyunsaturated fatty acids for use in, e.g. pharmaceutical

PT compositions, nutritional compositions, cosmetics or animal feed

PS Example 12; Pages 124-126; 165pp; English.

CC The present sequence is a human desaturase enzyme. The cDNA sequence was

CC identified based on homology between human cDNA sequences and Mortierella

CC alpina desaturase gene sequences. The specification describes methods for

CC desaturating a fatty acid and for producing a desaturated fatty acid by

CC expressing increased levels of a desaturase. The enzyme can be used for

CC desaturating fatty acids. The enzyme can be used to produce

CC polyunsaturated fatty acids, which can be used for treating malnutrition,

CC in pharmaceutical compositions, in cosmetics or in animal feed. The

CC polyunsaturated fatty acids can be used for treating e.g. restenosis

CC after angioplasty, inflammation, rheumatoid arthritis, asthma,

CC psoriasis, cancer, diabetes or eczema or reduce blood pressure. They

CC can also be used to inhibit platelet aggregation, cause vasodilation,

CC lower cholesterol levels, inhibit proliferation of vessel wall smooth

CC muscle and fibrous tissue, reduce or prevent gastro-intestinal bleeding

CC and other side effects caused by non-steroidal anti-inflammatory drugs,

CC prevent or treat endometriosis and premenstrual syndrome, treat myalgic

CC encephalomyelitis and chronic fatigue after viral infections, treat

CC AIDS, multiple sclerosis, acute respiratory syndrome, hypertension and

CC inflammatory skin disorders.

CC Sequence 746 AA;

Query Match 18.5%; Score 421.5; DB 1; Length 746;

Best Local Similarity 28.1%; Pred. No. 1e-40;

Matches 119; Conservative 72; Mismatches 177; Indels 55; Gaps 13;

QY 11 LQLEMTQVDVSNVWVHFGGAEIENYQGRDADFVWVHFGAEADK-----LKRMPK 63

Db 24 LVIDRKVYNISEFTTRHFGGSSVISHYAGQDATDFVAFHINKGLVKYMNLSLIGELSP 83

QY 64 INPSFELPPQAAVNAQEDFRKRLRELIATGMDASPLWYSKI-----STTLGLGV 115

Db 84 EQPFE---PTKNELTDEFRELATVEMGLMKANHFVFLYLHILLDGAALTLWV 140

QY 116 LGYFLMVOYMYFIVGAVLLGMHYQ-QMGWLSHDICHQTFKRNWNVNLVGLVEGNGLOGF 174

Db 141 FG-----TSFLPFLCAVLLSVAQQAAGNLQHDYGHLSVYRKPKNHNLVHKFVIGHLKGA 196

QY 175 SVTCWKDRHNAHSATNVQGHDPDIDNLPPLAWSDDVTRASPI--SRKLIQF-----Q 226

Db 197 SANWNHRRHFQHHAKPNIFHKDPDVNKLHVFVLGE-----WQPIEYGGKKLKLPLYNHQH 251

QY 227 QIYFLV-ICILLRFIWCFCQVLTVRSCLKDRDNQFYRSQYKKEAIGALHWTALKALPHLFF 285

Db 252 EYFFLIGPLLPIMFYQYQIIMT-----IVHKNVVDLAWAVSYVIRFFITY 298

QY 286 MP--SILTSLLVFFVSELVGGGCIATVFMNHYPLEKIGDPVWDGHGFSVGQIHEMNIR 343

Db 299 IFPYGLGALLFLNFRFIESHWFWVTQNNHIVMEIDQAYRD--WFS-SQTATCNVE 355

QY 344 RGIITDWFEGGLNQYQIEHLLWPTLPRNLTAVSQVQEOQLCKHNLPRNPLPHEGLVILL 403

Db 356 QSFENDWFSGHLNFQIEHLLFPTMPRNLHKLAPLVKSLCAKHGIEYQEKPLALLDII 415

QY 404 RVL 406

Db 416 RSL 418

RESULT 10

W85135

ID W85135 standard; Protein: 746 AA.

AC W85135;

DE A desaturase enzyme encoded by contig 253538a.

KW Fatty acid; desaturase; polyunsaturated fatty acid;

KW malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis;

KW cancer; diabetes; eczema; platelet aggregation; vasodilation;

KW cholesterol level; endometriosis; premenstrual syndrome;

KW myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;

KW acute respiratory syndrome; hypertension; inflammatory skin disorder.

OS Homo sapiens.

EH Key

FT Misc_difference 746

FT /note= "not specified"

PN W09846765-A1.

PD 22-OCT-1998.

PF 10-APR-1998: U07422.

PR 11-APR-1997: US-833610.

PA (ABBO) ABBOTT LAB.

PA (CALJ) CALGENE LLC.

PI Chaudhary S, Huang Y, Knutzon D, Leonard AE, Mukerji P,

PI Thurmond J;

DR WPI: 99-009334/01.

DR N-PSDB: V82642.

PT New nucleic acid encoding delta5 and other desaturase enzymes -

PT useful in production of oils of increased arachidonic acid content,

PT used, e.g. for treating cancer, as foods, animal feeds and cosmetics

PS Claim 87; Pages 119-120; 153pp; English.

CC The present sequence represents a human desaturase enzyme. The enzyme

CC sequence is used in the methods of the invention. The specification

CC describes methods for desaturating a fatty acid and for producing a

CC desaturated fatty acid by expressing increased levels of a desaturase.

CC The enzyme can be used for desaturating fatty acids. The enzyme can be

CC used to produce polyunsaturated fatty acids, which can be used for

CC treating malnutrition, in pharmaceutical compositions, in cosmetics or

CC in animal feed. The polyunsaturated fatty acids can be used for treating

CC e.g. restenosis after angioplasty, inflammation, rheumatoid arthritis,

CC asthma, psoriasis, cancer, diabetes or eczema or reduce blood pressure.

CC They can also be used to inhibit platelet aggregation, cause

CC vasodilation, lower cholesterol levels, inhibit proliferation of vessel

CC wall smooth muscle and fibrous tissue, reduce or prevent

CC gastro-intestinal bleeding and other side effects caused by non-steroidal

CC anti-inflammatory drugs, prevent or treat endometriosis and premenstrual

CC syndrome, treat myalgic encephalomyelitis and chronic fatigue after

CC viral infections, treat AIDS, multiple sclerosis, acute respiratory

CC syndrome, hypertension and inflammatory skin disorders.

CC Sequence 746 AA;

chilling resistance; oilseed.
KW Borago officinalis.
OS Key Location/Qualifiers
FH Region 156..163
FT /label= Lipid_box
FT region 196..200
FT /label= Metal_box-1
FT region 372..377
FT /label= Metal_box-2
PN W09621022-A2.
PD 11-JUL-1996.
PF 28-DEC-1995; IB1167.
PR 30-DEC-1994; US-366779.
PA (RHON) RHONE POULENC AGROCHIMIE.
PI Freyssinet GL, Nuccio M, Nunberg AN, Reddy AS, Thomas TL;
DR WPI: 96-333997/33.
DR N-PSDB: T30395.
PT transgenic plants comprising the borage delta-6-desaturase gene
PT show increased production of gamma linolenic acid and having
PT increased resistance to chilling
PS Claim 3: Page 52-53: 75pp; English.
CC Borage delta-6-desaturase (R98455) catalyses the conversion of
CC linoleic acid to gamma-linolenic acid (GLA). Its sequence was
CC deduced from that of the delta-6-desaturase gene (T30395) isolated
CC from a borage membrane-bound polysomal library. The sequence is
CC distinct from that of Synecocystis delta-6-desaturase (R98456).
CC Expression of the desaturase in transgenic plants, esp. sunflower,
CC soybean, maize, tobacco, peanut, carrot or oilseed rape, results in
CC increased GLA prodn. Alteration of the plant membrane lipids as a
CC result of expression of the desaturase may also result in increased
CC resistance to chilling.
SQ Sequence 448 AA;

Query Match 19.3%; Score 439.5; DB 1; Length 448;
Best Local Similarity 30.0%; Pred. No. 3.6e-43;
Matches 122; Conservative 67; Mismatches 166; Indels 51; Gaps 14;
QY 11 LQLMQETVDVSAWVNFHFGGAEIENYOGRDATDAFVWVHFQEAEDKLRMPKINPSPEL 70
DB 25 ISIQKAYDVSDWVNDHFGGSPPLKSLAGQEVTDFAVAFHASTW---KNLDKFTGYL 81
QY 71 PQAANVDAQEDFRKRLRELIATGMFDA-----SPLWYSYKISTTLGLVGLGYFLWVQY 124
DB 82 -KDSVSEVSKDYRLKLVFEFSKMGLYDKKGIMFATLCF---IAMLFMSVYGVLFCEGV 137
QY 125 QMYIGAVLLGMHQQMGWLSHDICHQTFKRNMMNNLVGLVFGNGLQGSFVTCWKDRHN 184
DB 138 LVHLFSGCLMGFLWQSGWIGHGAGHYMVVSDSLNFKFMGIFAANCLSGISIGMKWKNHN 197
QY 185 AHSATNVQGHDPDIDNLPPLAWS-----EDDVTRASPISRKLIQFOQYYFLV 232
DB 198 AHTACNSLEYPDLOQVIFLVWSKFGSTSHFYERKLTDFS--LSRFFVSYQHWTFYP 256
QY 233 ICILLRFIWCQCVLTVRSKDRDNQFVRSQYKKEAIGLALHWTLLKALFLHFEMPISILTS 292
DB 257 IMCAARLNMVQSLI---MLLTKNVSYRAQ---ELLCG-----LVFSWY--PLVLS 301
QY 293 LL-----VFFVSELVGGFGIAIVVF--MNHYPLE-KIGDPVWDGHGFSVGOIHETMNI 344
DB 302 CLPNWGERIMFVIASLVTGMQQQVQFSLNHFSSSVYVGP--KGNMFEKTDGTDLTDLISC 359
QY 345 GIITDWFEGGLNVOIEHLLWPTLRPHNLTAVSQVEOLCQKHNL 390
DB 360 PPWMDWFHGLQFOIEHLLFPKMPRCNLRKISPYVIELCKHNL 405

RESULT 6
W67471
ID W67471 standard; Protein; 448 AA.
AC W67471;
DT 02-MAR-1999 (first entry)
DE Borage delta-6 desaturase protein.

Upstream region; regulatory region; sunflower; albumin; seed; expression;
KW Borago officinalis.
OS Key Location/Qualifiers
FH Region 40..44
FT /note= "cytochrome b5 haem-binding motif"
FT Domain 156..163
FT /note= "His-rich metal binding motif"
FT Domain 196..200
FT /note= "His-rich metal binding motif"
FT Domain 373..377
FT /note= "His-rich metal binding motif"
PN W09845460-A1.
PD 15-OCT-1998.
PF 09-APR-1998; U07178.
PR 09-APR-1997; US-831570.
PA (RHON) RHONE-POULENC AGROCHIMIE.
PI Beremand PD, Nunberg AN, Thomas TL;
DR WPI: 98-583201/49.
DR N-PSDB: V34398.
PT New sunflower albumin 5' regulatory region - useful for directing
PT altered lipid metabolism in plant seeds
PS Example 2: Fig 1: 38pp; English.
CC This sequence corresponds to the borage (Borago officinalis) delta-6
CC desaturase enzyme. The encoding lipid metabolism gene is an example
CC of a heterologous gene which can be expressed at high levels in a
CC seed-specific manner in transgenic plants, when placed under control
CC of the sunflower albumin gene 5' regulatory region (V34397).
SQ Sequence 448 AA;

Query Match 19.3%; Score 439.5; DB 1; Length 448;
Best Local Similarity 30.0%; Pred. No. 3.6e-43;
Matches 122; Conservative 67; Mismatches 166; Indels 51; Gaps 14;
QY 11 LQLMQETVDVSAWVNFHFGGAEIENYOGRDATDAFVWVHFQEAEDKLRMPKINPSPEL 70
DB 25 ISIQKAYDVSDWVNDHFGGSPPLKSLAGQEVTDFAVAFHASTW---KNLDKFTGYL 81
QY 71 PQAANVDAQEDFRKRLRELIATGMFDA-----SPLWYSYKISTTLGLVGLGYFLWVQY 124
DB 82 -KDSVSEVSKDYRLKLVFEFSKMGLYDKKGIMFATLCF---IAMLFMSVYGVLFCEGV 137
QY 125 QMYIGAVLLGMHQQMGWLSHDICHQTFKRNMMNNLVGLVFGNGLQGSFVTCWKDRHN 184
DB 138 LVHLFSGCLMGFLWQSGWIGHGAGHYMVVSDSLNFKFMGIFAANCLSGISIGMKWKNHN 197
QY 185 AHSATNVQGHDPDIDNLPPLAWS-----EDDVTRASPISRKLIQFOQYYFLV 232
DB 198 AHTACNSLEYPDLOQVIFLVWSKFGSTSHFYERKLTDFS--LSRFFVSYQHWTFYP 256
QY 233 ICILLRFIWCQCVLTVRSKDRDNQFVRSQYKKEAIGLALHWTLLKALFLHFEMPISILTS 292
DB 257 IMCAARLNMVQSLI---MLLTKNVSYRAQ---ELLCG-----LVFSWY--PLVLS 301
QY 293 LL-----VFFVSELVGGFGIAIVVF--MNHYPLE-KIGDPVWDGHGFSVGOIHETMNI 344
DB 302 CLPNWGERIMFVIASLVTGMQQQVQFSLNHFSSSVYVGP--KGNMFEKTDGTDLTDLISC 359
QY 345 GIITDWFEGGLNVOIEHLLWPTLRPHNLTAVSQVEOLCQKHNL 390
DB 360 PPWMDWFHGLQFOIEHLLFPKMPRCNLRKISPYVIELCKHNL 405

RESULT 7
W98130
ID W98130 standard; Protein; 448 AA.
AC W98130;
DT 21-JUN-1999 (first entry)
DE Borage delta-6 desaturase.
KW Delta-6 desaturase; borage; oleosin; AtS21; promoter;
KW transgenic plant; seed; lipid; fatty acid; oilseed; vegetable oil;
KW gamma-linolenic acid; octadecatetraenoic acid.

PF	10-APR-1998; U07126.
PR	11-APR-1997; US-834655.
PA	(ABBO) ABBOTT LAB.
PA	(CALJ) CALGENE LIC.
PI	Chaudhary S, Huang Y, Knutzon D, Leonard AE, Mukerji P,
PI	Thurmond J;
DR	WPI: 98-594582/50.
PT	New-Isolated fatty acid desaturase enzymes - used for the production
PT	of polyunsaturated fatty acids for use in, e.g. pharmaceutical
PT	compositions, nutritional compositions, cosmetics or animal feed
PS	Example 2; Pages 101-102; 165pp; English.
CC	The present sequence represents a peptide derived from a desaturase
CC	enzyme. The specification describes methods for desaturating a
CC	fatty acid and for producing a desaturated fatty acid by expressing
CC	increased levels of a desaturase. Desaturases can be used for
CC	desaturating fatty acids. The enzymes can be used to produce
CC	polyunsaturated fatty acids, which can be used for treating malnutrition,
CC	in pharmaceutical compositions, in cosmetics or in animal feed. The
CC	polyunsaturated fatty acids can be used for treating e.g. restenosis
CC	after angioplasty, inflammation, rheumatoid arthritis, asthma, psoriasis,
CC	cancer, diabetes or eczema or reduce blood pressure. They can also be
CC	used to inhibit platelet aggregation, cause vasodilation, lower
CC	cholesterol levels, inhibit proliferation of vessel wall smooth muscle
CC	and fibrous tissue, reduce or prevent gastro-intestinal bleeding and
CC	other side effects caused by non-steroidal anti-inflammatory drugs,
CC	prevent or treat endometriosis and premenstrual syndrome, treat myalgic
CC	encephalomyelitis and chronic fatigue after viral infections, treat AIDS,
CC	multiple sclerosis, acute respiratory syndrome, hypertension and
CC	inflammatory skin disorders.
SO	Sequence 355 AA;

used to inhibit platelet aggregation, cause vasodilation, lower cholesterol levels, inhibit proliferation of vessel wall smooth muscle cells, reduce or prevent gastro-intestinal bleeding and fibrous tissue, reduce or prevent anti-inflammatory, other side effects caused by non-steroidal anti-inflammatory, prevent or treat endometriosis and premenstrual syndrome, encephalomyelitis and chronic fatigue after viral infections, multiple sclerosis, acute respiratory syndrome, hypertension, inflammatory skin disorders.

Sequence 355 AA;

CC prevent or treat endometriosis and premenstrual syndrome, treat myalgia
CC encephalomyelitis and chronic fatigue after viral infections, treat A
CC multiple sclerosis, acute respiratory syndrome, hypertension and
CC inflammatory skin disorders.
SQ Sequence 355 AA;

CC multiple sclerosis, acute respiratory syndrome, hypertension and
CC inflammatory skin disorders.
SQ Sequence 355 AA;

50 Sequence 355 AA;

Model	Best Local Similarity	Pred. No.	3.9e-58
Model 1	34.9%	34.9%	34.9%
Model 2	34.9%	34.9%	34.9%
Model 3	34.9%	34.9%	34.9%
Model 4	34.9%	34.9%	34.9%
Model 5	34.9%	34.9%	34.9%
Model 6	34.9%	34.9%	34.9%
Model 7	34.9%	34.9%	34.9%
Model 8	34.9%	34.9%	34.9%
Model 9	34.9%	34.9%	34.9%
Model 10	34.9%	34.9%	34.9%
Model 11	34.9%	34.9%	34.9%
Model 12	34.9%	34.9%	34.9%
Model 13	34.9%	34.9%	34.9%
Model 14	34.9%	34.9%	34.9%
Model 15	34.9%	34.9%	34.9%
Model 16	34.9%	34.9%	34.9%
Model 17	34.9%	34.9%	34.9%
Model 18	34.9%	34.9%	34.9%
Model 19	34.9%	34.9%	34.9%
Model 20	34.9%	34.9%	34.9%
Model 21	34.9%	34.9%	34.9%
Model 22	34.9%	34.9%	34.9%
Model 23	34.9%	34.9%	34.9%
Model 24	34.9%	34.9%	34.9%
Model 25	34.9%	34.9%	34.9%
Model 26	34.9%	34.9%	34.9%
Model 27	34.9%	34.9%	34.9%
Model 28	34.9%	34.9%	34.9%
Model 29	34.9%	34.9%	34.9%
Model 30	34.9%	34.9%	34.9%
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Model 32	34.9%	34.9%	34.9%
Model 33	34.9%	34.9%	34.9%
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Model 41	34.9%	34.9%	34.9%
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Model 67	34.9%	34.9%	34.9%
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Model 72	34.9%	34.9%	34.9%
Model 73	34.9%	34.9%	34.9%
Model 74	34.9%	34.9%	34.9%
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Model 80	34.9%	34.9%	34.9%
Model 81	34.9%	34.9%	34.9%
Model 82	34.9%	34.9%	34.9%
Model 83	34.9%	34.9%	34.9%
Model 84	34.9%	34.9%	34.9%
Model 85	34.9%	34.9%	34.9%
Model 86	34.9%	34.9%	34.9%

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RESULT 5

ID	R98455 standard; Protein; 448 AA.
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DT 15-SEP-1996 (first entry)

Delta-6-desaturase; gamma-linolenic acid; transgenic plant; borage;
KW

THE UNIVERSITY OF CHICAGO PRESS

QY 111 LGLVGLGYFLMVOYOM-----YFIGAVLLGMHYOQMGWLSHDICHOTKNNNNLVL 165
 Db 132 LCIWGLSTVIVAKWGOTSTLANVLSAALLGLFWOQCGWLAHDFLHHQVQDFRFGWDLFGA 191
 QY 166 VFGNGLOGFVTCWDRHNAHSATNVQGHDPDIDNPLPLAWSDDVTRASPI----- 219
 Db 192 FLGGVCGGFSWKKHNTTHAAPNVHGEDPDIDTHTPLTWSEHALEMESDVPDELT 251
 QY 219 --SRKLIQOQYVFLVICILLRFTWCFOCVLTVRSKLDKRDNQYRSQYK-----BAIG 270
 Db 252 MWSRFVNLQNTWYFPLSPARLSWCLQSILFVLP-----NGQAHKPSGARVPISLVEQLS 307
 QY 271 LALHWTLKALFLHFFMPSILTSLLVFEVSELVGGFGIAIVFMNHYPLEKIGDPVWDG 330
 Db 308 LAHWHTWYLATMFLFKDPVNMVLYFVLSQVCGNLLAIVFSLNHNMGFVISEEAVDMD 367
 QY 331 FSVGQIHEHMTNRGIIITDFFGGLNYQIEHHLWTLPRHNLTAVSQVQEQCLCKHNL 390
 Db 368 FETKQIITGRDHPGLFANFTGGLNYQIEHHLFSPMRHNFESKIOPAVETLCKKNVRY 427
 QY 391 RNPPLPHEGLVILLRYLAVFARMAEKOPA-----GKA 421
 Db 428 HTTGMEGTGTA-----EVFSRLNEVSKAASKMGKA 456

RESULT 2
 W95504
 ID W95504 standard; peptide: 457 AA.
 AC W95504;
 DT 26-MAR-1999 (first entry)
 DE Mortierella alpina delta 6 desaturase.
 KW Delta 6 desaturase; recombinant; fatty acid desaturase; FAD; PUFA; oil;
 KW polyunsaturated fatty acid; linoleic acid; arachidonic acid; linolenic;
 KW stearidonic acid; eicosapentaenoic acid; malnutrition; feeding formula;
 KW dietary supplement; prostaglandin; restenosis; angioplasty; inflammation;
 KW rheumatoid arthritis; psoriasis; osteoporosis; cancer; eczema; AIDS;
 KW diabetes; cosmetic; animal feed.
 OS Mortierella alpina.
 PN W09846764-A1.
 PD 22-OCT-1998.
 PF 10-APR-1998; U07421.
 PR 24-OCT-1997; US-956985.
 PR 11-APR-1997; US-833610.
 PR 11-APR-1997; US-834033.
 PR 11-APR-1997; US-834855.
 PA (ABBO) ABBOTT LAB.
 PA (CALJ) CALGENE LLC.
 PI Chaudhary S, Huang Y, Knutzon D, Leonard AE, Mukerji P,
 PI Thurmond J;
 DR WPI: 99-080739/07.
 DR N-PSDB: X00889.
 PT Nucleic acid construct able to express fatty acid desaturase in
 PT plants - useful in human or animal nutrition, as cosmetics and
 PT therapeutically, e.g. for restenosis, cancer and diabetes
 PS Claim 7; Fig 3A-E; 210pp; English.
 CC This represents a Mortierella alpina delta 6 desaturase. The invention
 CC relates to a nucleic acid construct that contains at least one of the
 CC nucleotide sequences (X00889 to X00891) encoding M. alpina delta 6,
 CC delta 12 and delta 5 desaturases (W95504 to W95506) respectively, coupled
 CC to an expression control sequence functional in plants. Recombinant plant
 CC cells containing at least one DNA encoding a M. alpina fatty acid
 CC desaturase (FAD), can be used for the production of polyunsaturated fatty
 CC acid (PUFA). These recombinant cells or plants containing them are used
 CC to produce oils such as linoleic acid, arachidonic acid, gamma-linolenic
 CC acid, dihomo-gamma-linolenic acid, stearidonic acid and eicosapentaenoic
 CC acid (EPA). These plant oils are used: (i) to treat malnutrition; (ii) in
 CC infant feeding formulas, or dietary supplements or substitutes, for use
 CC in humans or animals; (iii) for treating disorders associated with
 CC inadequate consumption or production of PUFA (or their metabolites such
 CC as prostaglandins), e.g. restenosis after angioplasty, inflammation,
 CC AIDS, rheumatoid arthritis, psoriasis, osteoporosis, cancer, eczema,
 CC diabetes; (iv) as cosmetics, and (v) as animal feeds. Fragments of the

CC DNA are used as probes to isolate related coding sequences. Recombinant
 CC plants can produce high yields of PUFA, since new pathways can be created
 CC and unwanted ones suppressed. Plants can be engineered to express oils of
 CC particular PUFA composition, e.g. one similar to that in human milk, and
 CC product recovery is simpler than with e.g. fish.
 SQ Sequence 457 AA;

Query Match 27.6%; Score 631; DB 1; Length 457;
 Best Local Similarity 33.0%; Pred. No. 9.5e-66;
 Matches 150; Conservative 76; Mismatches 173; Indels 56; Gaps 11;

QY 2 KSKRQALSPLOLM--EQTYDVSNAVNFHFGGABIIENYQGRDATDAPVWVHFOEAFDKL 59
 Db 23 EGKDAEAPFLMIIDNKVDYDFEVPDPHFGS-VILTHVGKDGTDVDTFHPAAWETL- 81
 QY 60 RMPKINPSPFLPQAAVNEAQEDF-----RKLEELIATGMEDASPLWYSKISTT 110
 Db 81 -----ANFVV---GDIDESDRDIKNDDFAAEVRKLTFLFQSLGYDSSKAYTAKVSN 131
 QY 111 LGLVGLGYFLMVOYOM-----YFIGAVLLGMHYOQMGWLSHDICHOTKNNNNLVL 165
 Db 132 LCIWGLSTVIVAKWGOTSTLANVLSAALLGLFWOQCGWLAHDFLHHQVQDFRFGWDLFGA 191
 QY 166 VFGNGLOGFVTCWDRHNAHSATNVQGHDPDIDNPLPLAWSDDVTRASPI----- 219
 Db 192 FLGGVCGGFSWKKHNTTHAAPNVHGEDPDIDTHTPLTWSEHALEMESDVPDELT 251
 QY 219 --SRKLIQOQYVFLVICILLRFTWCFOCVLTVRSKLDKRDNQYRSQYK-----BAIG 270
 Db 252 MWSRFVNLQNTWYFPLSPARLSWCLQSILFVLP-----NGQAHKPSGARVPISLVEQLS 307
 QY 271 LALHWTLKALFLHFFMPSILTSLLVFEVSELVGGFGIAIVFMNHYPLEKIGDPVWDG 330
 Db 308 LAHWHTWYLATMFLFKDPVNMVLYFVLSQVCGNLLAIVFSLNHNMGFVISEEAVDMD 367
 QY 331 FSVGQIHEHMTNRGIIITDFFGGLNYQIEHHLWTLPRHNLTAVSQVQEQCLCKHNL 390
 Db 368 FETKQIITGRDHPGLFANFTGGLNYQIEHHLFSPMRHNFESKIOPAVETLCKKNVRY 427
 QY 391 RNPPLPHEGLVILLRYLAVFARMAEKOPA-----GKA 421
 Db 428 HTTGMEGTGTA-----EVFSRLNEVSKAASKMGKA 456

RESULT 3
 W85121
 ID W85121 standard; Protein; 457 AA.
 AC W85121.
 DT 11-FEB-1999 (first entry)
 DE A delta-6 desaturase enzyme amino acid sequence.
 KW Fatty acid; delta-6 desaturase; polyunsaturated fatty acid;
 KW malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis;
 KW cancer; diabetes; eczema; platelet aggregation; vasodilation;
 KW cholesterol level; endometriosis; premenstrual syndrome;
 KW myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;
 KW acute respiratory syndrome; hypertension; inflammatory skin disorder.
 OS Unidentified.
 PN W09846765-A1.
 PD 22-OCT-1998.
 PF 10-APR-1998; U07422.
 PR 11-APR-1997; US-833610.
 PA (ABBO) ABBOTT LAB.
 PA (CALJ) CALGENE LLC.
 PI Chaudhary S, Huang Y, Knutzon D, Leonard AE, Mukerji P,
 PI Thurmond J;
 DR WPI: 99-009334/01.
 DR New nucleic acid encoding delta5 and other desaturase enzymes -
 DR useful in production of oils of increased arachidonic acid content.
 PT used, e.g. for treating cancer, as foods, animal feeds and cosmetics
 PS Disclosure: Pages 95-96; 153pp; English.
 CC The present sequence represents a fatty acid delta-6 desaturase enzyme.
 CC The specification describes methods for desaturating a fatty acid and

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OM protein - protein search, using sw model

Run on: February 25, 2000, 04:45:46 ; Search time 38.64 Seconds
(without alignments)
258.684 Million cell updates/sec

Title: PCT-US99-28655-4
Perfect score: 2283
Sequence: 1 MKSKRQALSPQLMEQTYDV.....LRYLAVFARMAEKOPAGKAL 422

Scoring table: BLOSUM62

Searched: 188963 seqs, 23686106 residues

Database : A_Geneseq_36.*

Word size : 0

Number of hits that pass the threshold : 188963

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	631	27.6	457	1	W84137	A delta-6 desaturase
2	631	27.6	457	1	W95504	Mortierella alpina
3	622	27.2	457	1	W85121	A delta-6 desaturase
4	565	24.7	355	1	W84139	Desaturase enzyme
5	439.5	19.3	448	1	R98455	Borage delta-6-des
6	439.5	19.3	448	1	W67471	Borage delta-6 des
7	439.5	19.3	448	1	W88130	Borage delta-6 des
8	430.5	18.9	446	1	W85122	A delta-6 desaturase
9	421.5	18.5	746	1	W84156	Human desaturase e
10	421.5	18.5	746	1	W85135	A desaturase enzyme
11	421.5	18.5	753	1	W95514	Amino acid sequenc
12	310	13.6	608	1	W84155	Human desaturase e
13	310	13.6	608	1	W85134	A desaturase enzyme
14	310	13.6	615	1	W95513	Amino acid sequenc
15	277.5	12.2	252	1	W84141	Desaturase enzyme
16	249.5	10.9	446	1	W85119	A delta-5 desaturase
17	249.5	10.9	446	1	W95506	Mortierella alpina
18	247	10.8	555	1	W84154	Human desaturase e
19	247	10.8	555	1	W85133	A desaturase enzyme
20	247	10.8	562	1	W95512	Amino acid sequenc
21	244	10.7	306	1	W84153	Human desaturase e
22	244	10.7	306	1	W85132	A desaturase enzyme
23	244	10.7	306	1	W95511	Amino acid sequenc
24	239	10.5	359	1	R34102	Bacterial delta-6-
25	239	10.5	359	1	R98456	Synechocystis delt
26	239	10.5	359	1	W85123	A delta-6 desaturase
27	218	9.5	365	1	W85124	A delta-6 desaturase
28	200	8.8	131	1	W84143	Desaturase enzyme
29	185	8.1	211	1	W84151	Human desaturase e
30	185	8.1	211	1	W85130	A desaturase enzyme
31	185	8.1	218	1	W95509	Amino acid sequenc
32	176	7.7	143	1	W84145	Desaturase enzyme
33	175	7.7	140	1	W84149	Schizochytrium sp.
34	175	7.7	140	1	W85128	A putative partial
35	175	7.7	140	1	W95518	M. alpina desaturase
36	152	6.7	87	1	W81144	Desaturase enzyme
37	148	6.5	382	1	W31740	Delta-12 desaturase
38	147	6.4	312	1	W95095	Synechocystis sp.
39	144.5	6.3	418	1	R60501	Linoleic-acid-desa

Sequence of soybean
Microsomal delta-1
Amino acid sequenc
Phaeodactylum tric
A putative desatur
Fatty acid desatur

40 140 6.1 379 1 R53699
41 138.5 6.1 384 1 W24998
42 138.5 6.1 384 1 W94050
43 138 6.0 102 1 W84147
44 138 6.0 102 1 W85126
45 138 6.0 102 1 W95516

ALIGNMENTS

RESULT 1

W84137

ID W84137 standard; Protein; 457 AA.

AC W84137;

DE 15-FEB-1999 (first entry)

DW A delta-6 desaturase enzyme.

KW Fatty acid; delta-6 desaturase; polyunsaturated fatty acid;

KW malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis;

KW cancer; diabetes; eczema; platelet aggregation; vasodilation;

KW cholesterol level; endometriosis; premenstrual syndrome;

KW myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;

KW acute respiratory syndrome; hypertension; inflammatory skin disorder.

OS Mortierella alpina.

PN W09846763-A1.

PD 22-OCT-1998.

PF 10-APR-1998; U07126.

PR 11-APR-1997; US-834655.

PA (ABBO) ABBOTT LAB.

PA (CALJ) CALGENE LLC.

PI Chaudhary S, Huang Y, Knutson D, Leonard AE, Mukerji P,

PI Thurmond J;

DR WPI; 98-594582/50.

DR N-PSDB; V63624.

PT New isolated fatty acid desaturase enzymes - used for the production

PT of polyunsaturated fatty acids for use in, e.g. pharmaceutical

PT compositions, nutritional compositions, cosmetics or animal feed

PS Claim 3; Fig 3A-E; 165pp; English.

CC The present sequence represents a Mortierella alpina fatty acid delta-6

CC desaturase enzyme. The enzyme sequence is used in the methods of

CC the invention. The specification describes methods for desaturating a

CC fatty acid and for producing a desaturated fatty acid by expressing

CC increased levels of a desaturase. The present desaturase is an enzyme

CC which introduces a double bond carbons 6 and 7 from the carboxyl end of

CC a fatty acid molecule. The enzyme can be used for desaturating fatty

CC acids. The enzyme can be used to produce polyunsaturated fatty acids,

CC which can be used for treating malnutrition, in pharmaceutical

CC compositions, in cosmetics or in animal feed. The polyunsaturated fatty

CC acids can be used for treating e.g. restenosis after angioplasty,

CC inflammation, rheumatoid arthritis, asthma, psoriasis, cancer, diabetes

CC or eczema or reduce blood pressure. They can also be used to inhibit

CC platelet aggregation, cause vasodilation, lower cholesterol levels,

CC inhibit proliferation of vessel wall smooth muscle and fibrous tissue,

CC reduce or prevent gastro-intestinal bleeding and other side effects

CC caused by non-steroidal anti-inflammatory drugs, prevent or treat

CC endometriosis and premenstrual syndrome, treat myalgic encephalomyelitis

CC and chronic fatigue after viral infections, treat AIDS, multiple

CC sclerosis, acute respiratory syndrome, hypertension and inflammatory skin

CC disorders.

SQ Sequence 457 AA;

Query Match 27.6%; Score 631; DB 1; Length 457;

Best Local Similarity 33.0%; Pred. No. 9.5e-66;

Matches 150; Conservative 76; Mismatches 173; Indels 56; Gaps 11;

OY 2 KSKRQALSPQLM--EQYDVSAWVNFHPGGAEIENYOCRDATDAFWVHQRQADKLK 59

DB 23 EGKDKAEAPFLMIIDKNKYDVFDPDPHGGGS-VILTHVKGDTGDTDFDFHPEAAWETL 81

OY 60 RMPKINPSFELPQQAQVNAQEDF-----RKLRELIATGMFDASPLWYSKYIST 110

DB 81 -----ANFYV---GDIDESDRDINDPFAAEVRKLTFLFQSLGYDSSKAYAFKVSFN 131

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OY 392 TMRHNLNTVMPVKFEAAANGLPY 416
Db 390 TMRHNLHKLAPLVKSLCAKHGIEY 414

RESULT 15
Q920R9 PRELIMINARY; PRT; 444 AA.
AC Q920R9;
DT 01-MAY-1999 (TMRHNLrel. 10, Created)
DT 01-MAY-1999 (TMRHNLrel. 10, Last sequence update)
DT 01-NOV-1999 (TMRHNLrel. 12, Last annotation update)
DE DELTA-6 FATTY ACID DESATURASE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE; 99085046.
RA CHO H.P., NAKAMURA M.T., CLARKE S.D.;
RT "Cloning, expression, and nutritional regulation of the mammalian
RL Delta-6 desaturase.";
DR EMBL; AF126798; AAD20017.1; -.
DR HSSP; P00171; 3B5C.
SQ SEQUENCE 444 AA; 52387 MW; F6F9668B CRC32;

Query Match 15.3%; Score 373; DB 11; Length 444;
Best Local Similarity 25.8%; Pred. No. 4.9e-24;
Matches 124; Conservative 68; Mismatches 179; Indels 110; Gaps 17;

OY 4 REQEHPEFFIKIDKWCODDAVL-----RSHPGG-SAITTYKNMDATTVFHTFGSK 56
Db 22 RWEEIQKHNLTQ-RWLVDRKYNVTKWSQRHGVGHYSGEDATDAFRAHLDLD 80
OY 57 EAYQWLTELK-KECPTQPEIPDKDDPIKIGDDVNMGTFNISEKRSQAINKSFIDLRMR 115
Db 81 FVGKFLKPLLGELAPEP-----SLDRCKSSQITDFALAKT 119
OY 116 VRAEGLMDGSLFYRKILETIFILFAFYL--QYHTYLP---SAILMGVAMQOLGWL 170
Db 120 AEDNLFKTNHLLFFLLSHIIVMESLAWFILSYFGTGWIPTLVTAFLVATSOAAGWLQ 179
OY 171 HEFAHOLFKNRYNDLASVYGVNFGLOGFSSGKKEOHNVHHAATNVVGRDGLDLVPFY 230
Db 180 HDYGHLSVYKSIWNVVHKFVIGHLKGSANWNNHRFQHHAKPNIFHKDPDI----- 234
OY 231 ATVAEHLNYSQDSWVMTLFRWQ-----HVHWTFML---PFLRLSWLIQS 272
Db 234 -----KSLHVFVLGEMQPLEYGGKKLKYLPYNNHQHEYFELIGPPLL----- 275
OY 273 IIFVSQMPHTHYDYRTAIYEQVGLSHWAMSLGQLYFLPDNSTRIMFF-LVSHLVG-- 330
Db 275 -----IPMYFQYQIIMTISRDRWDVLAWAIS----YIMRFFTYIIPFYGILGALVFN 324.
OY 330 --GFLLSH---VTFNHYSVEKALSNSNIMSNYACIQIMTRNMRPGRFIDNLWGGLNY 383
Db 325 FIRELESNFWVWQMNHLVNE---IDLHYRDMFSSQAAATCNVEOSFFDNFSGHLNF 381
OY 384 QIEHHLFPTMRHNLNTVMPVKFEAAANGLPYVVDYFTGFWELEIOFRNIANVAKLT 443
Db 382 QIEHHLFPTMRHNLHKLAPLVKSLCAKHGIEY-----EKPLLRALIDIVSSLK 431
OY 444 K 444
Db 432 K 432

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Qy 129 ----YIRKILETIFILFAFYLO-----YHTYILPSAILMGVAAQOGLWLTHEFAH 175
Db 127 ERVGHTPKFLAVAMSVLFIALCYVLACSSGTAHMF---AGGLGFIWISQWIGHDSGH 183
Qy 176 HOLFKRNYNDLASVYFNGFLOGSSGGWKQKHNVHHAATNVVGRDGLDLVPFFATVAE 235
Db 184 HOITRHPALNLLQVYVSGNCLTGLGIAMWKNHNTHHISCSNLDHDPDLQHLPLFAVSTK 243
Qy 236 HLNYSQDSWMTL-----FRQHVHWF--MLPELRLSWLLSIIF--VSQMTHTYD 285
Db 244 LFNLMNSVCYERTLAFDAISAEFFSYQHWTFYPVNGFARINLLVOSIVFLITQKV---- 300
Qy 286 YIRNTAIYEQVGLSLHNAWSLGQLYFLPDWSTRIMEFLVSHLVGGFLLSHV-VTPNHYSV 344
Db 300 ---RQRWEIAGVAAFWYVYPLLVSCLENWVERVAFVLAFFVITG--IQHVQFCLNHFSS 354
Qy 345 EKFASSNIMSNYACLOIMTTRNMRPGRFIDWLAGGLNYQIEHHLFTPMRHNLTVMPL 404
Db 355 AVY-VGPPKGNDFEROTAGTLDIKCSPMDMDFHGGLOFQVEHHLFPRLPRCHYRWVAPI 413
Qy 405 VKEFAAANGLPY 416
Db 414 VRDLCKKHGLSY 425

RESULT 13
Q92RP8 ID Q92RP8 PRELIMINARY; PRT; 449 AA.
AC Q92RP8;
DT 01-MAY-1999 (TremBLrel. 10, Created)
DT 01-MAY-1999 (TremBLrel. 10, Last sequence update)
DT 01-NOV-1999 (TremBLrel. 12, Last annotation update)
DE DELTA-8 SPHINGOLIPID DESATURASE.
GN SLD1.
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
OC Brassica.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. DRAKKAR; TISSUE=RIPENING EMBRYOS;
RX MEDLINE; 99003197.
RA SPERLING P., ZAEHRINGER U., HEINZ E.;
RT "A sphingolipid desaturase from higher plants. Identification of a new
cytochrome b5 fusion protein.";
RL J. Biol. Chem. 273:28590-28596(1998).
DR EMBL; AJ224160; CAA11857.1; -.
DR HSSP; P00173; 1AQA.
DR MENDEL; 34704; Brana;2419;34704.
SQ SEQUENCE 449 AA; 51490 MW; F9BB69EE CRC32;
```

```
Query Match 15.5%; Score 378.5; DB 10; Length 449;
Best Local Similarity 24.9%; Pred. No. 1.7e-24;
Matches 109; Conservative 84; Mismatches 173; Indels 71; Gaps 17;

Qy 5 BOEHEP--FFKIDGKWCQIDDAVLRSHPGG-SAITYKNMDATTVFHTFTGSKAEYQW 61
Db 16 KKHNPQGLWISIQGVYDVSHV-KSPGGGAAILNLAGQVDTAFIAHPGT----AW 70
Qy 62 LTELKKECTOPEIPIDKDDPIKGDVNMGTFTNISEKRSQKSFDTLDRMVRAGEL 121
Db 71 -----RHLENLHG-YHVKHVSDVSRYRLAAEFKRCGL 106
Qy 122 MDGSPFLYIRKILETIFT-LEAFYLYQHTY-----YLPsAILMGVAAQOGLWLI 170
Db 107 FD-----KKGHTVLTITCVAAALAAVYGVVACTSIWAHLISAVLLGLLWISQAYG 159
Qy 171 HEFAHOLFKNRYNDLASVYFNGFLOGSSGGWKQKHNVHHAATNVVGRDGLDLVPY 230
Db 160 HDSGHYNTSTKPCNKVQLLSGNCITGISIAWKNWTHNAHISCSNLDHDPDLOHIPVL 219
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Qy 231 ATVAEHLNNYSQDSWMTL-----FRQHVHWFMTLPEL---RLSWLLSIIFVSOMP 280
Db 220 AVSNKFKFSMTSREYGRKLTEDPLAREFLISYQHSF-YPIKCVGRINFIOTLLLSFR- 278
Qy 281 THYDYIRNTAIYEQVGLSLHNAWSLGQLYFLPDWSTRIMEFLVSHLVGGFLLSHV-VTF 339
Db 278 RYVDRALNIA-----GILVFWTWFPPLVSLFPMOERLIIFVLSMAYTA--IQHVQCL 330
Qy 340 NHYSVEKFASSNIMSNYACLOIMTTRNMRPGRFIDWLAGGLNYQIEHHLFTPMRHNLT 399
Db 331 NHFAADVYTGPPN-GNDWFKEQTAGTLDISCRSYMDWFFGGLOFQLEHHLFPRLPRCHLR 389
Qy 400 TVMPLVKEFAAANGLPY 416
Db 390 GVSPPVQELCKKHNLPI 406

RESULT 14
O95864 ID O95864 PRELIMINARY; PRT; 444 AA.
AC O95864;
DT 01-MAY-1999 (TremBLrel. 10, Created)
DT 01-MAY-1999 (TremBLrel. 10, Last sequence update)
DT 01-NOV-1999 (TremBLrel. 12, Last annotation update)
DE DELTA-6 FATTY ACID DESATURASE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 99085046.
RA CHO H.P., NAKAMURA M.T., CLARKE S.D.;
RT "Cloning, expression, and nutritional regulation of the mammalian
Delta-6 desaturase.";
RL J. Biol. Chem. 274:471-477(1999).
DR EMBL; AF126799; AAD20018.1; -.
DR HSSP; P00171; IWDB.
SQ SEQUENCE 444 AA; 52259 MW; 78230925 CRC32;
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Query Match 15.4%; Score 374.5; DB 4; Length 444;
Best Local Similarity 26.5%; Pred. No. 3.7e-24;
Matches 118; Conservative 70; Mismatches 166; Indels 91; Gaps 17;

Qy 6 QEHEPFFIKIDGKWCQIDDAVLRL-----SHPGGS-AITYKNMDATTVFHTFTGSKEA 58
Db 27 QKHN---LRTD-RWLVIDRKVYNITKWSIQHPGGQGVGHYAGEDATDAFRAFPDLFV 82
Qy 59 YOWLT-----ELKKECTOPEIPIDKDDPIKGDVNMGTFTNISEKRSQKINQSFDTLR 113
Db 83 GKFLKPLLIGELAPEPSQD-----HGKSKITEDFRALR 117
Qy 114 MRVRAEGMDGSPFLYIRKI-----LETI--FTILFAFYLYQHTYLP---SAILMGVAV 163
Db 118 KTAEDMNLFKNVHVFLLLLLAHIALESIAFTV---FY--FGNWIPLTITAFVLATSQ 172
Qy 164 QOLGLWLIHEFAHOLFKNRYNDLASVYFNGFLOGSSGGWKQKHNVHHAATNVVGRDGD 223
Db 173 AQAGWLQHDYGHLSVYRKPKNHLVHKFVIGHLKASANWNNHRRFQHHAKNFIHKDPD 232
Qy 224 LDLVFPYATVAEHLNNYSQDSWMTLFRQHVHWTMFLPFLRLSWLLSIIFVSQMTHTY 283
Db 233 VNMLHVFVGEWQPTGYGKKLKYLPYNHQHEHYFFLPGPLLPYFOYIIM----- 286
Qy 284 YDYIRNTAIYEQVGLSLHNAWSLGQLYFLPDWSTRIMEFLVSHLVGG-----FLSH 335
Db 286 -----THIVKKNWDLAWVS---YIRFEITYIPFY---GILGALLFLNFIREFLESH 332
Qy 336 ----YVTNHYSVKEFALSSNIMSNYACLOIMTTRNMRPGRFIDWLAGGLNYQIEHHLFP 391
Db 333 WFWVTQNHVME---IDQENYRDFWFSQLTATCNVEQSFENDFSGHLNFQIEHHLFP 389
```


OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC	core eudicots; Asteridae; euasterids II; Asterales; Asteraceae;
OC	Asteroidae; Heliantheae; Helianthus.
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN-CV. INBRED LINE HA89, SE163 /91;
RC	TISSUE-COTYLEDONS OF DEVELOPING SUNFLOWER FRUITS;
RX	MEDLINE: 96028121.
RC	SPELTING P.; SCHMIDT H.; HEINZ E.;
RT	"A cytochrome-b5-containing fusion protein similar to plant acyl lipid
RT	desaturases".
RL	Eur. J. Biochem. 232:798-805(1995).
DR	EMBL: X87143; CAA60621.1; -.
DR	HSSP: P00171; IWD8.
DR	MNDEL: 8443; Helan; 2419;8443.
DR	PFAM: PF00173; heme_1; 1.
SO	SEQUENCE 458 AA; 52231 MW; FA2AE27B CRC32;

Query Match	16.5%	Score	402.5;	DB	10;	Length	458;
Best Local Similarity	24.8%	Pred. No.	1.5e-26;				
Matches	113;	Conservative	89;	Mismatches	184;	Indels	69;
Gaps							
Qy	12	FIKIDGKCWCI	DDAVLRSHPGGSA-	ITTYKNM	DAATVFHTFHTGS	KEAYQWLTELK	KECP 70
Db	34	WISLGRVYN	TEWA-KEH	PGGDAPL	NLAGQDV	DAFIAPG	T-----AW----- 80
Qy	71	TQPEEIP	DIKDDPKIG	DDVNM	GFTNISEK	RSQAQIN	KSTFTDLRMVRAEGLMDGS----- 126
Db	80	-----	-----	-----	-----	-----	-----
Qy	126	PLFYIR	KILET-IFT	ILF--	AFVLYQ	VHTYTP	LSAISLGMVAWQOLGLWLI
Db	125	YSLCFV	SLLSACV	GVLYSG	SFWI----	-----	-----
Qy	182	RYNDLAS	YVGNLQ	FGSSG	WKEQ	NVHHAAT	NVVGROGDLDPFYFATVAEHLNNYS 241
Db	180	RGWNKE	AGIFIG	NCITGIS	IAWKKWT	NAHHIA	CNSLDYDPDLQHLPLMAVSSKLFNSIT 239
Qy	242	Q-----	-----	-----	-----	-----	-----
Db	240	SVFGR	OLTDP	LARFFV	SQHYLYY	IPMCVARN	LYLQITILLISKRKIPD-----RG 293
Qy	290	TAIYQ	VGLSL	HWAWS	LGOLY	FLPDW	STRIMFFVLVSHLVGGFLLSHV-VTFNYSVEKFA 348
Db	294	LNI---	LGTLIF	WTFPL	LSRLPN	PWPVAF	VLVSCVTG--IQHIQFTLNHFSGDV- 348
Qy	349	LSSNMS	NYACLO	ITMTR	NRPGF	IDWL	NGLNQYQIEHLLFTPMRHNLTWYPLVKEF 408
Db	348	VGPPK	GNWPEK	QPRGR	ITDIT	IACSS	MMWDFGGQFQLEHLLFPLRPLCHLRSISPICREL 407
Qy	409	AAANG	PLYM	VDDYD	YTFG	WLEIEQ	PRNTANYAAKIT 443
Db	408	CKKNY	LPVSL	SYFD	ANVT	LKTLRT	AAOARDLT 442

RESULT	9	
Q9ZRP7		
ID	Q9ZRP7	PRELIMINARY;
AC	Q9ZRP7	PRT; 449 AA.
DT	01-MAY-1999	(TREMBlrel. 10, Created)
DT	01-MAY-1999	(TREMBlrel. 10, Last sequence update)
DT	01-NOV-1999	(TREMBlrel. 12, Last annotation update)
DE	DELTA-8 SPHINGOLIPID DESATURASE.	
GN	SD1.	
OS	Arabis thaliana (Mouse-ear cress).	
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
OC	euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;	
OC	core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;	
OC	Arabidopsis.	
RP	[1]	
RP	SEQUENCE FROM N.A.	

RC STRAIN-CV. COLUMBIA;
RX TISSUE-MAINLY GREEN PARTS, SOME FLOWERS, FEW ROOTS;
RC MEDLINE; 99003197.
RX
RA SPERLING P., ZAEHRINGER U., HEINZ E.;
RT "A sphingolipid desaturase from higher plants. Identification of a new
RT cytochrome b5 fusion protein."; *J. Biol. Chem.* 273:28590-28596(1998).
RL
DR ENBL; AJ224161; CAA11858.1; "-"
DR HSSP; P00171; LWDB.
DR MENDEL; 34619; Arath;2419;34619.
SQ SEQUENCE 449 AA; 51675 MW; 36C26D4D CRC32;

Query Match	16.5%	Score 402;	DB 10;	Length 449;
Best Local Similarity	24.6%;	Pred. No. 1.7e-26;		
Matches 114;	Conservative	81;	Mismatches 186;	Indels 82;
Gaps				
Qy	12	FIKDGKWCQIDDAVLRSHPGG-SAITYKNMDATVFHTFHFGSKEAYQWLTELKKECP 70		
Db	25	WIALQGVYVNSDWI-KTHPGGDTVLNLVQGDVDAFIAFHPT--AWHHLDL----- 77		
Qy	71	TQPEEIPDIKDDPIKIDDVNMGTFNISEKRSQAIKNSITDLRMVRVRAGLMD--GSPLEF 128		
Db	77	-----FTGYHIDRFQVSEVDYRMAAEFKLGLFENKGHVTL 115		
Qy	129	YIRKILETIF-----TILFAFVLOVHTYLYPSAILMGVAMQOLGWLHEFAHHOL 178		
Db	116	YTLAFVAAFLGVLYGLACTSVFAHQI-----AAALLGLLTQSAYIGHDSGHYVI 167		
Qy	179	FKNRYNDLASYPVGNFLQFGSSGKWKEQHNHVHAATNVVGRDGLDLVPFYATVAEHLN 238		
Db	168	MSNKSYNRFQALLSGNCLTGISIAWKWKTHNAHLACNSLDYDPDLQHIPVFAVSTKFFS 227		
Qy	239	NYSQ-----DSWVMTLFRHQVHVTFMLPFLRLSMLQSIIEV---SOMPTHYDY 286		
Db	228	SLRSRFYDRKLITDPVAVRFLVSQHHTYYPVCMFCGINLFIQTFLLLSKREVPDRALNF 287		
Qy	287	YRNTAIYEQYGLSLHNAWSLGQLYFLPDLWSTRIIMFFLVSHLGGFLLSHV-VTFNHYSVE 345		
Db	288	-----AGILVFTWTFPLLYSCLPNWPERRFFVFTSFTVTA--LQHIQFTLNHFAAD 336		
Qy	346	KEALSSNIMSNYACLOIMTTRNNRPGCFRITDLWGLGGLNYQIEHHLFTPTMRPHNLNTVPLV 405		
Db	337	VY-VGPTGSDWEKQAAGTIDICRSYDWDFFGGLOFQLEHHLFPRLPRLPCHLRKRVSPVV 395		
Qy	406	KEFAAANGLPYVDDYFTGFWLEIE-----QFRNIANVAAK 441		
Db	396	OELCKKNLPLRYSNWSFEANVLINTLKTAAYQARDVAPVVK 438		

RESULT	10
O60427	PRELIMINARY; PRT; 444 AA.
ID	
AC	O60427;
DT	01-AUG-1998 (TEmBLrel. 07, Created)
DT	01-AUG-1998 (TEmBLrel. 07, Last sequence update)
DT	01-NOV-1999 (TEmBLrel. 12, Last annotation update)
DE	BC269730.2.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
OC	Eutheria; Primates; Catarrhini; Hominoidea; Homo.
RN	[1]
RP	SEQUENCE FROM N.A.
RA	LAMERDIN J.E., MCCREARY P.M., COLEMAN M., SKOWRONSKI
RA	BURKHART-SCHULZ K., GORDON L., KYIE A., RAMIREZ M.
RA	PHAN H., VELASCO N., DO L., REGALA W., TERRY A., GA
RA	DANGANAN L., POUNDSTONE P., CHRISTENSEN M., GEORGE
RA	LIU S., ATTIX C., ANDREISE T., FRANKHEIM M., AMICO-P
RA	COEFIELD J., DUARTE S., LUCAS S., BRUCE R., THOMAS F
RA	KRONWILLER B., ARELLANO A., MONTGOMERY M., OW D., NO
RA	KOBAYASHI A., OLSEN A.S., CARRARO A.V.;
RL	Submitted (May1998) to the EMBL/GenBank/DDBJ databa
DR	EMBL: AC004770. AAC23397.1.

QY 181 NRYNDLASTYFVGNFLOGSSGGWKEQHNHHAATNVVGRDGLDLPFYATVAEHLNNY 240
 DB 181 NRYNDLASTYFVGNFLOGSSGGWKEQHNHHAATNVVGRDGLDLPFYATVAEHLNNY 240
 QY 241 SODSWMTLFRWQHVHTFMLPFLRLSWLQSIIFVSQMPHYDYRYNTAIYEQVGLSL 300
 DB 241 SODSWMTLFRWQHVHTFMLPFLRLSWLQSIIFVSQMPHYDYRYNTAIYEQVGLSL 300
 QY 301 HWASISGLQFLPDWSTRIMFFLVSHLVGGFLLSHVTFNHYSEKFAISNINACL 360
 DB 301 HWASISGLQFLPDWSTRIMFFLVSHLVGGFLLSHVTFNHYSEKFAISNINACL 360
 QY 361 QIMTRNMRGRFIDWLWGLGNYOIEHHLFPTMPRHNLNTVMPVKEFAAANGLPYVDD 420
 DB 361 QIMTRNMRGRFIDWLWGLGNYOIEHHLFPTMPRHNLNTVMPVKEFAAANGLPYVDD 420
 QY 421 YFTGFWEIEQFRNIANVAALKTKKIA 447
 DB 421 YFTGFWEIEQFRNIANVAALKTKKIA 447
 RESULT 2
 Q94044 PRELIMINARY; PRT; 454 AA.
 AC Q94044;
 DT 01-FEB-1997 (T-EMBLrel. 02, Created)
 DT 01-FEB-1997 (T-EMBLrel. 02, Last sequence update)
 DT 01-JAN-1999 (T-EMBLrel. 09, Last annotation update)
 DE T13F2.1 PROTEIN.
 OS T13F2.1.
 GN Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
 OC Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA SWINBURNE J.;
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 94150718.
 RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M., COULSON A.,
 RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., FULTON L.,
 RA CRAYTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
 RA GARDNER A., GREEN P., HAKINS T., HILLIER L., JIER M., JOHNSTON L.,
 RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
 RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
 RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
 RA SMAILDON N., SMITH A., SONNHAMMER E., STADEN R., SULTON J.,
 RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
 RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans.";
 RL Nature 368:32-38(1994).
 DR EMBL; 281122; CAB03352.1;
 SQ SEQUENCE 454 AA; 53160 MW; D7FD13FA CRC32;

Query Match 99.4%; Score 2421.5; DB 5; Length 454;
 Best Local Similarity 98.5%; Pred. No. 4.2e-199;
 Matches 447; Conservative 0; Mismatches 0; Indels 7; Gaps 1;
 QY 1 MYLREQEHPFIKIDGKWCQDDAVLRSHPGGSAITTYKNMDATTVFHTFGSKEAYQ 60
 DB 1 MYLREQEHPFIKIDGKWCQDDAVLRSHPGGSAITTYKNMDATTVFHTFGSKEAYQ 60
 QY 61 WLTELKKECTOPEIPDKDDPIKIDGIDVNMGTFTNISEKRSQAINKSTDLRMVRAEG 120
 DB 61 WLTELKKECTOPEIPDKDDPIKIDGIDVNMGTFTNISEKRSQAINKSTDLRMVRAEG 120
 QY 121 LMDGSPFYIRKILETIFTILFAFYLYQHTYLLPSAILMGVAQQQLGWLHIEFAHHQLEK 180
 DB 121 LMDGSPFYIRKILETIFTILFAFYLYQHTYLLPSAILMGVAQQQLGWLHIEFAHHQLEK 180

QY 181 NRYNDLASTYFVGNFLO-----GFSSGGWKEQHNHHAATNVVGRDGLDLPFYATV 233
 DB 181 NRYNDLASTYFVGNFLOSHIFNNGFSSGGWKEQHNHHAATNVVGRDGLDLPFYATV 240
 QY 234 AEHLNNYSQDSWMTLFRWQHVHTFMLPFLRLSWLQSIIFVSQMPHYDYRYNTAIY 293
 DB 241 AEHLNNYSQDSWMTLFRWQHVHTFMLPFLRLSWLQSIIFVSQMPHYDYRYNTAIY 300
 QY 294 EQVGLSLHWASISGLQFLPDWSTRIMFFLVSHLVGGFLLSHVTFNHYSEKFAISNIN 353
 DB 301 EQVGLSLHWASISGLQFLPDWSTRIMFFLVSHLVGGFLLSHVTFNHYSEKFAISNIN 360
 QY 354 MSNTACLOIMTRNMRGRFIDWLWGLGNYOIEHHLFPTMPRHNLNTVMPVKEFAAANG 413
 DB 361 MSNTACLOIMTRNMRGRFIDWLWGLGNYOIEHHLFPTMPRHNLNTVMPVKEFAAANG 420
 QY 414 LPYVDDYFTGFWEIEQFRNIANVAALKTKKIA 447
 DB 421 LPYVDDYFTGFWEIEQFRNIANVAALKTKKIA 454
 RESULT 3
 O61388 PRELIMINARY; PRT; 443 AA.
 AC O61388;
 DT 01-AUG-1998 (T-EMBLrel. 07, Created)
 DT 01-AUG-1998 (T-EMBLrel. 07, Last sequence update)
 DT 01-NOV-1998 (T-EMBLrel. 08, Last annotation update)
 DE DELTA6-FATTY-ACID-DESATURASE.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
 OC Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 97268723.
 RA SAYANOVA O., SMITH M.A., LAPINSKAS P., STOBART A.K., DOBSON G.,
 RA CHRISTIE W.W., SHEWRY P.R., NAPIER J.A.;
 RT "Expression of a borage desaturase cDNA containing an N-terminal
 RT cytochrome b5 domain results in the accumulation of high levels of
 RT delta6-desaturated fatty acids in transgenic tobacco.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:4211-4216(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 98149727.
 RA NAPIER J.A., HEY S.J., LACEY D.J., SHEWRY P.R.;
 RT "Identification of a Caenorhabditis elegans Delta6-fatty-acid-
 RT desaturase by heterologous expression in Saccharomyces cerevisiae.";
 RL Biochem. J. 330:0-0(0).
 DR EMBL; AF031477; AAC15586.1;
 SQ SEQUENCE 443 AA; 51740 MW; EE44468D CRC32;

Query Match 44.9%; Score 1092.5; DB 5; Length 443;
 Best Local Similarity 46.3%; Pred. No. 1.6e-85;
 Matches 201; Conservative 84; Mismatches 140; Indels 9; Gaps 4;

QY 13 IKIDGKWCQDDAVLRSHPGGSAITTYKNMDATTVFHTFGSKEAYQVHTLKKECPTQ 72
 DB 12 MKVDGKNLYSELVKKHPGGAIVQYRNSDATHIFAFHEGSSQAQKOLDLLKRGHEHD 71
 QY 73 EPEIPDKDDPIKIDGIDVNMGTFTNISEKRSQAINKSTDLRMVRAEGMDGSPFYI 130
 DB 72 E-----FLEKQLEKRLDKVDINVSAYDSVAQEKKNVSEKLEKRLQKLDHDLGKANEYFL 127
 QY 131 RLITETIFILFAFYLYQHTYLLPSAILMGVAQQQLGWLHIEFAHHQLEKFNRYNDLASY 190
 DB 128 FKAISTLSIMAFAYLYQHTYLLPSAILMGVAQQQLGWLHIEFAHHQLEKFNRYNDLASY 187
 QY 191 FYGNFLQFSSGGWKEQHNHHAATNVVGRDGLDLPFYATVAEHLNNY--SODSWMT 248
 DB 188 FFGNFLQFSSGGWKEQHNHHAATNVVGRDGLDLPFYATVAEHLNNY--SODSWMT 247

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OM protein - protein search, using sw model

Run On: February 24, 2000, 22:03:17 ; Search time 51.75 Seconds
(without alignments)
598.886 Million cell updates/sec

Title: PCT-US99-28655-2
Perfect score: 2435
Sequence: 1 MVLREQHEPFFIKDGKWC.....ETQPRNIANVAALTKKIA 447

Scoring table: BLOSUM62

Searched: 225878 seqs, 69334122 residues

Database : SPTREMBL_12:*

Word size : 0

Number of hits that pass the threshold : 225878

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2435	100.0	447	5 Q9XTB7	Q9xtb7 caenorhabdi
2	2421.5	99.4	454	5 Q94044	Q94044 caenorhabdi
3	1092.5	44.9	443	5 O61388	O61388 caenorhabdi
4	1073.5	44.1	473	5 Q23221	Q23221 caenorhabdi
5	578.5	23.8	525	10 Q92NW2	Q92nw2 physcomitre
6	422.5	17.4	449	10 Q82348	Q82348 arabidopsis
7	412.5	16.9	448	10 Q04353	Q04353 borago offi
8	402.5	16.5	458	10 Q43469	Q43469 hellanthus
9	402	16.5	449	10 Q92RP7	Q92rp7 arabidopsis
10	401.5	16.5	444	4 O60427	O60427 homo sapien
11	397	16.3	446	10 Q92TY9	Q92ty9 ricinus com
12	390.5	16.0	469	10 Q92T08	Q92t08 triticum ae
13	378.5	15.5	449	10 Q92RP8	Q92rp8 brassica na
14	374.5	15.4	444	4 Q95864	Q95864 homo sapien
15	373	15.3	444	11 Q920R9	Q920r9 mus musculu
16	372.5	15.3	445	4 Q9V500	Q9v5q0 homo sapien
17	367	15.1	444	11 Q92122	Q92122 ratus norv
18	364.5	15.0	446	10 Q92T29	Q92tz9 arabidopsis
19	316.5	13.0	311	4 Q9Y3X4	Q9y3x4 homo sapien
20	266.5	10.9	345	2 Q9X8W4	Q9x8w4 streptomyce
21	241	9.9	467	5 Q96099	Q96099 dictyosteli
22	231	9.5	446	3 Q74212	Q74212 mortierella
23	216.5	8.9	464	5 Q9Y1W0	Q9y1w0 dictyosteli
24	211	8.7	368	2 Q54795	Q54795 spirulina p
25	173	7.1	352	4 O60426	O60426 homo sapien

26	152.5	6.3	332	10 Q9ZPH4	Q9zph4 arabidopsis
27	150	6.2	379	10 Q22628	Q22628 arachis hyp
28	149.5	6.1	287	8 O19891	O19891 cyanidium c
29	144.5	5.9	352	2 O34653	O34653 bacillus su
30	142	5.8	385	10 Q23955	Q23955 gossypium h
31	141.5	5.8	312	10 Q92NW8	Q92nw8 brassica ra
32	140.5	5.8	427	2 O05874	O05874 mycobacteri
33	140.5	5.8	379	10 O65772	O65772 crepis pala
34	140	5.7	361	2 O85776	O85776 rhizobium l
35	139.5	5.7	347	2 Q55231	Q55231 synechococc
36	138	5.7	387	10 Q41131	Q41131 ricinus com
37	137	5.6	383	10 Q41305	Q41305 solanum com
38	137	5.6	383	10 Q23956	Q23956 gossypium h
39	136.5	5.6	359	2 Q55240	Q55240 synechocyst
40	133	5.5	362	3 O59715	O59715 schizosacch
41	132.5	5.4	384	10 O81094	O81094 lequerella
42	132	5.4	323	4 O15121	O15121 homo sapien
43	131.5	5.4	378	10 Q24499	Q24499 hellanthus
44	131.5	5.4	384	10 Q92PI2	Q92pi2 brassica ce
45	131	5.4	350	2 Q44503	Q44503 anabaena va

ALIGNMENTS

RESULT	1				
Q9XTB7					
ID	Q9XTB7	PRELIMINARY;	PRT;	447 AA.	
AC	Q9XTB7;				
DT	01-NOV-1999 (TREMBLrel. 12, Created)				
DT	01-NOV-1999 (TREMBLrel. 12, Last sequence update)				
DT	01-NOV-1999 (TREMBLrel. 12, Last annotation update)				
DE	DELTA5-FATTY ACID DESATURASE.				
GN	FAT-4 OR DES-5.				
OS	Caenorhabditis elegans.				
OC	Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;				
OC	Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE; 99059458.				
RA	WATTS J.L., BROWSE J.:				
RT	"Functional identification of a fatty acid delta5 desaturase gene from				
RT	Caenorhabditis elegans."				
RL	Arch. Biochem. Biophys. 362:175-182(1999).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	SPECIES=C.elegans;				
RX	MEDLINE; 99059458.				
RA	MICHAELSON L.V., NAPIER J.A., LEWIS M., GRIFFITHS G., LAZARUS C.M.,				
RT	STOBBART A.K.:				
RT	"Functional identification of a fatty acid delta5 desaturase gene from				
RT	Caenorhabditis elegans."				
FEBS Lett.	439:215-218(1998).				
DR	EMBL; AF114440; RAD13294.1;				
DR	EMBL; AF078796; AAC93143.1;				
SQ	SEQUENCE 447 AA; 52348 MW; E62A9A02 CRC32;				

Query Match 100.0%; Score 2435; DB 5; Length 447;
Best Local Similarity 100.0%; Pred. NO. 2.9e-200;
Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MVLREQHEPFFIKDGKWCQIDAVLRSHPGGSAITTYKNMDATTVFHFTGSKYAY 60	
Db	1	MVLREQHEPFFIKDGKWCQIDAVLRSHPGGSAITTYKNMDATTVFHFTGSKYAY 60	
QY	61	WLTELKKECTQBPETDIDKDDPIKIGIDDYVMGTNFNISEKRSQAINKSFDTLNRVRAEG 120	
Db	61	WLTELKKECTQBPETDIDKDDPIKIGIDDYVMGTNFNISEKRSQAINKSFDTLNRVRAEG 120	
QY	121	LMGDSPLFYRKILETFTILFAFYLOHYHYLPSATLMGVAMQOLGWLHFEFAHQLFK 180	
Db	121	LMGDSPLFYRKILETFTILFAFYLOHYHYLPSATLMGVAMQOLGWLHFEFAHQLFK 180	

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Db 201 RPYDRFACHYDPYPIYNNR---ERLQIFISDAGVLGVCYLL-----YRIALVKGLAWL 251
Qy 328 -----VGGFL-----LSHV-VTFNHYSVEKFALSSNIMSNYACLOIMTTRNMRPG 371
Db 252 VCVYGVPLLVVNGFVLITYLQHTHPSLPHYDSTEW-----288
Qy 372 RFIDWLWGGL-----NYQIEHHLEFTMPRHN-----LNTVMPLVKFEFA 409
Db 288 ---DWLRLGALATCDRDYGVNLKVFHNITDTHVYVHHLESTWPHYNAMEATKAVKELLGDYY 344
Qy 410 AANGLPYMVDYFTGFWEIEQ 431
Db 345 QFDGTP-----IYKEMWREAKE 361
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Search completed: February 24, 2000, 22:01:38
Job time: 17315 sec

Query Match	5.6%	Score 137;	DB 2;	Length 383;
Best Local Similarity	21.5%;	Pred. No. 0.00078;		
Matches	82;	Conservative 38;	Mismatches 112;	Indels 150; Gaps 21;
QY	130	IRKLEITETILFAFLQY--HYV--LPSSALLMGVAAQQLGWL-----	THEF	173
		: : : : : : : : : : : : : : : : : : : :		
Db	50	IRSFVYVDLILVSIWYVANTIFHLPLSPYCV-IAW-FYIWTCCGCVCTGIWVNAHEC	107	
QY	174	AHOLFKNRYND-----LASYFVGNFLQGS GGWKEQHNHYHAATNVVGRGD	223	
		: : : : : : : : : : : : : : : : : : : :		
Db	108	GHAESDYQWDDTVGLLHSALLVPYF-----SMKYSHRRHHSNTGSLERDEV	156	
QY	224	LDLVP-----FYATVAEHLNNYSQDSWVMTLFRQHVHTFMPLFLLSLWLLQSIIFVSQ	278	
		: : : : : : : : : : : : : : : : : : : :		
Db	157	FVPKPSQLGWY---SKYLNPNPGRVLSLPI-----TTLTGLMPLYLAFNVSG	200	
QY	279	MP-----THYDYD---YRNTAIEQVGLSLSHWAWSLGOLYFLPDWSTRIWFFLVSHL---	328	

A:Reference number: 216895
 A:Accession: T09880
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-385 <LIU>
 A:Cross-references: EMBL:X97016; NID:e991751; PID:242368
 A:Experimental source: cultivar Deltapine-16
 C:Function:
 A:Description: Introduces a cis double bond at omega-6 position of oleic acids
 C:Superfamily: omega-3 fatty acid desaturase

Query Match 5.8%; Score 142; DB 2; Length 385;
 Best Local Similarity 19.2%; Pred. No. 0.0003;
 Matches 85; Conservative 56; Mismatches 119; Indels 182; Gaps 22;
 QY 83 PIKIDVNMGT-----FNISKRSA-----QINKST-----DLRVRVREG 120
 DB 8 PIDGIKENRGVNRVPIEKPPFTLGQIKQAIKPHCFRRSLRFSYVVDLCL----- 62
 QY 121 LMDGSPFYIRKILETITILFAF-----YLOVHTY-LPSAILMGVAVQOLGWL-HE 172
 DB 62 -----ASFYY-----TATSFHFLPQPFVIANPVVWLOGCILTGV-----WVIAHE 105
 QY 173 FAHOLFKNRYND-----LASFYVGNFLQFSGGKKEQHNHHAATNVGRDG 222
 DB 106 WGHAFRDYQWVDDTVGLILHSALLVPYF-----SWKISHRRHSNTGSMERDE 154
 QY 223 DLDLVP--FYATVAEHLNNYSQDSNVWTLFRQVHVTMPLPFLRLSLWLLQSLIFVSOMP 280
 DB 155 VFVPKPKSKLSCFAKYLNN--PPGRVSLVTLTGLGWPMLAF-----NVS 198
 QY 281 THYD-----YVRNTAIVEQVGLSLHAWMSLQGLYFLPDWSTRI 319
 DB 199 GRYDRLASHNPNPGPIYSRDRLOVYISDGFIVAVVLYKIAATKGLAWLLCYGVPL 258
 QY 320 MFFLVSHLVGGFLSHVYTF-----NHYSVEKFASSNIMSNYACLIQMTTRMRPG 371
 DB 259 L-----IVNAFLV--LITYLQHTSALPHYDSSW----- 287
 QY 372 RFIDWLWGLL-----NYQIEHLFTMPHNN-----LNTVMPVLKFEA 409
 DB 287 ---DWLRGALSTMDRDFGLNKNVFNHNTDTHVAHHLFTMPHYHAMEATKAIRPILGYY 343
 QY 410 AANGLPYVMDYFTGFWEIEQ 431
 DB 344 PFDGTP-----IYKAWREAKE 360

RESULT 11
 G70590
 Probable desA3 protein - Mycobacterium tuberculosis (strain H37Rv)
 C:Species: Mycobacterium tuberculosis
 C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 17-Jul-1998
 C:Accession: G70590
 R:Cooper, S. T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Cole, S. T.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Connor, R. A.; Rogers, J.; Rutter, S.; Seeger, K. K.; Skelton, S.; Squares, S.; Rajandream, M. A.; Rogers, J. Nature 393, 537-544, 1998
 A:Authors: Squares, R.; Sulston, J. E.; Taylor, K.; Whitehead, S.; Barrell, B. G.
 A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
 A:Reference number: A70500; MUID:98295987
 A:Accession: G70590
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-427 <COL>
 A:Cross-references: GB:A1123456; NID:g3261742; PID:e314467; PID:g2072696
 A:Experimental source: strain H37Rv
 C:Genetics:
 A:Gene: desA3
 Query Match 5.8%; Score 140.5; DB 2; Length 427;

Best Local Similarity 20.9%; Pred. No. 0.00046;
 Matches 52; Conservative 46; Mismatches 134; Indels 17; Gaps 6;
 QY 200 SSGGWKEQHN-VHHAATNVYGRDGLDLPFYATVAEHLNNYSQDSWMTLFRQVHVT 258
 DB 117 SSKHRYTHNFVHKYINILGMDDDVGVLVRTRDQKWKRYNIFNVVNTILAIGFEWG 176
 QY 259 FMLPFLRLSLWLLQSLIFVSQMPHYDYRYNT---AIYEQVGLSLHAWMSLQGLYFLPDW 315
 DB 177 VALQHLTEIGTKIFKGRADREAKTRLEFSKAGROVFKDYVAFPALTSLSPGATY----- 232
 QY 316 STRIMFVLVSHLVGGFLSHVVTENHY--SVEKFALSSNI---MSNYACLIQMTTRMRP 370
 DB 232 RSTIANVAVANVNVNSNAVFCGHPDGAETKTDMICEPKQWTLRQWLSANENA 291
 QY 371 GRFDLWGLGGLNYQIEHLFTMPRHNLNTVMPVLKFAAANGLPYVDDYFTGFWEIE 430
 DB 292 GPALRFMSGNLCHOIEHLXPDLPSNRLHEISVRREVCDYDLPTTGTGSLVQYG---K 348
 QY 431 QFRNIANVA 439
 DB 349 TWRTIAKLS 357
 RESULT 12
 S43771
 phosphatidylcholine desaturase (EC 1.3.1.35) - Synecococcus sp. (strain PCC 7002)
 N:Alternate names: Delta-12 desaturase; fatty acid desaturase (EC 1.14.99.-) (misc)
 C:Species: Synecococcus sp.
 A:Variety: PCC 7002
 C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 28-May-1999
 C:Accession: S43771
 R:Sakamoto, T.; Wada, H.; Nishida, I.; Ohmori, M.; Murata, N.
 Plant Mol. Biol. 24, 643-650, 1994
 A:Title: Identification of conserved domains in the Delta-12 desaturases of cyanob
 A:Reference number: S43770; MUID:94207189
 A:Accession: S43771
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-347 <SAK>
 A:Cross-references: GB:D13779; NID:g488510; PIDN:BAA02922.1; PID:d1003428; PID:g48
 C:Superfamily: omega-3 fatty acid desaturase
 C:Keywords: Oxidoreductase

Query Match 5.7%; Score 139.5; DB 2; Length 347;
 Best Local Similarity 21.0%; Pred. No. 0.00043;
 Matches 74; Conservative 54; Mismatches 151; Indels 73; Gaps 14;
 QY 110 TDLRMVRAEGLMDGSPFYIRKILETI-----FTIL 141
 DB 2 TSVTVRPSATTLLEKHPNLRDLTDLTPRSVYEINPLKWSRVLLSVAAVVGCYALLAI 61
 QY 142: FAFYLYQHYTYLPSAILMGVAVQOLGWL-HEFAHQHQLFKNRYNDLASYFVGNEL---Q 197
 DB 62 APWYLLPVWELTGTTLGTF-----FVIGDCGHSRFSKRNWNNLVGHILA--FLPLYI 113
 QY 198 GFSGCGKEQHNHHAATNVYGRDGLDLPFYATVAEHLNNYSQDSWMTLFRQVHVT 257
 DB 114 PFHS--WILHNHHRYN--NMEDNAWAPTPELYD-----DSPAFIKAVYR----- 159
 QY 258 TFMPLFLRLSLWLLQSLIFVSQMPHYDYRYNTAIYEQVGLSLHAWMSLQGL-----YF 311
 DB 159 ---AIRKGLMWLASVI--HOLKLHFNWFAFEGKQOVRFSALEFVITAGIAFAFPMFT 212
 QY 312 LPDWSTRIMFVLVSHLVGGFLSHVVTENHYSVEKFASSNIMSNYACLIQMTTRMRPG 371
 DB 213 LGVGVG-VKFWLMPWLVGHFWMS--TFTLVHHTVPEIPFSYRDKWNEAIAQLSGTVHCDYP 270
 QY 372 RFIDWLWGLNVOIEHLFTMPRHNLNTVMPVLKFAAANGLPYVDDYFT 423
 DB 271 KWVEVLCHDINVHPHHLSTGIPSYNLRKAYASIKQ----NWGEVLYETKFS 318

[illegible]

QY 249 LERMOHVHTFMLPFLRLSLWLSIIFFVSQMPHYYDYRNTAIYEQVGLSLHWASLQ 308
Db 125 PYHQHHEYFLGPPLLIPHYFOQIIM-----TMIHVKNVVDLAWAVS-- 169
QY 309 LYFLPDKWTRIMFLVSHLVGG-----FLLSH-----VVFNFHYVEKFASSNTMSN 356
Db 169 -YYIRFFITIPFY--GILGALLFLNFIRFLESHEWFWVTQMNHVME-----IDQEAIRD 221
QY 357 YACLOIMTNRMPGRFIDMLWGLNGLOIEHLEFPTPRHNLNTVMPVLEFAAANGLPY 416
Db 222 WFSQLPATCNQVQSFNDWFSGLHNFQIEHLEFPTPRHNLNLKIAPLVKSLCAKHGIEY 281

RESULT 5
S35157
Delta(6)-desaturase - Synechocystis sp.
C:Species: Synechocystis sp.
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 28-May-1999
C:Accession: S35157; S76243
R:Reddy, A.S.; Nuccio, M.L.; Gross, L.M.; Thomas, T.L.
Plant Mol. Biol. 22, 293-300, 1993
A:Title: Isolation of a Delta(6)-desaturase gene from the cyanobacterium Synechocystis sp.
A:Reference number: S35157; MUID:93283633
A:Accession: S35157
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-359 <RED>
A:Cross-references: GB:L11421; NID:9349562; PID:9349563
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, N. K.; 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp.
A:Reference number: S74322; MUID:97061201
A:Accession: S76243
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-359 <KAN>
A:Cross-references: EMBL:D90914; GB:AB001339; NID:g1653477; PID:d1019235; PID:g1653589
A:Experimental source: PCC 6803
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 8.7% Score 211; DB 2; Length 359;
Best Local Similarity 23.4%; Pred. No. 6.1e-10;
Matches 84; Conservative 62; Mismatches 147; Indels 66; Gaps 18;
QY 112 LRMVRA-----EGLMD-GSPLFYIRKILETITIFAFYLOYHTYLP-----SAIL 158
Db 19 LNRVDAYFAEHLGTQRDNPSMY-----LKTLLIWLFSAWAFVLFAPVFPVRLGCMV 74
QY 159 MGVAQOQLGWLIIHEFAHQLFKNRYNDLASVFNELQSGSGGKQKHQNH-VHHAATNV 217
Db 75 LAIALAFAFSFNVGDHANAYSSNPINRVLGMTYDFV-GUSSFWRVHRNVLHTYINI 133
QY 218 VGRGDL--DLVPFVATVAEHLNNYSQDSWVNTLFRQVH-VTFMPLFLRLSLWLSQII 274
Db 134 LGHDEVEHGDGAVRNSPQEHVG-----IVRFQOFYINGLYL-FIPFYFLYDYV 182
QY 275 FVSQMPHYDY-----YRNTAIYEQVGLSLHWASLQGLYFLPDWSTRIIMFLVSHLVGG 330
Db 183 LVLN-KGYHDKHKKIPFPQLELASLLGIKLLW---LGVVFGLP---LALGFSIPEVLGA 235
QY 331 -----FLLSHVVTFNHYVEKFASSNIMNSVACLOIMTNRMPGR-FID 375
Db 236 SVTYMTYGIIVCTIFMLAHVLESTEF-LTPDGESGAIDDEWAICOIRTNATNPFWN 294
QY 376 WLKGLNVOIEHHLFPPTPRHNLNTVMPVLEFAAANGLPYVVDYFTGF-----WLE 428
Db 295 WFCGGLNHQVTHLFPNICHYHPOLENIKDVCOEFGVEYKYVTFRAAIAASNYRWLE 353

RESULT 6

S54809
linoleoyl-CoA desaturase (EC 1.14.99.25) - Spirulina platensis
N:Alternate names: Delta6-desaturase
C:Species: Spirulina platensis
C:Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Sep-1997
C:Accession: S54809
R:Tasaka, Y.
submitted to the EMBL Data Library, May 1995
A:Reference number: S54809
A:Accession: S54809
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-368 <TAS>
A:Cross-references: EMBL:X87094; NID:9809109; PID:g809110
C:Keywords: oxidoreductase

Query Match 8.7% Score 211; DB 2; Length 368;
Best Local Similarity 24.3%; Pred. No. 6.3e-10;
Matches 90; Conservative 63; Mismatches 129; Indels 88; Gaps 21;
QY 111 LDRMRV-----RAEGL--MDGSPFLFYIRKILETITIFAFYLOYHTYI-----LP 154
Db 19 ELNRRVNAYLEAENISPRDNPPMY-----LKT--AILLAWVVSATVVFVGPDLVLMKIL 71
QY 155 SAILMGVAMQOQLGWLIIHEFAHQLFKNRYNDLASVFNELQSGSGGKQKHQNHV-HH 212
Db 72 GCIVLGFQVSAVGFNISHDGNGGYSQYQWNYLSG--LTHDAIGVSSYLKFRHNLVHH 129
QY 213 AATNVVGRDGL--DLVPFVATVAEHLNNYSQDSWVNTLFRQVH--VHW--TFMPLFLR 265
Db 130 TYTNILGHDEVEHGDVLRMSPE-----YRWHRYQHNVFWFYVPIIP 174
QY 266 LSULL--OSIIFVSQMPHYDYRNTAIYEQVGLSLHW-AWSLQGLYFLPDWSTRIIMF 321
Db 175 YNWSIADVQTMFLFRQ---YHDHEIPSPVVDIATLAFRAFGVAVFLIIP--IAGVY 227
QY 322 FLVSHLVGG-----FLLSHVVTFNHYVEKFASSN--TMSNVACLOIMTT 365
Db 228 SPLEAVIGASIVYVTHGLVACVWFMLAHI-----EPAEFLDPDLHIDDEWAIQAQVKT 282
QY 366 RNMPPGR-FIDMLWGLNGLOIEHLEFPTPRHNLNTVMPVLEFAAANGLPYVVDYFTG 424
Db 283 VDFAPNPIINWYVGLNYQTVVHLFPFHICHIHPKIPAIILAEVCEEFVNVAVHQTFFG 342
QY 425 -----FWLE 428
Db 343 ALAANYSLK 352

RESULT 7
T07687
omega-6 desaturase FAD2-1, microsomal - soybean
C:Species: Glycine max (soybean)
C:Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 26-Aug-1999
C:Accession: T07687
R:Heppard, E.P.; Kinney, A.J.; Stecca, K.L.; Miao, G.H.
Plant Physiol. 110, 311-319, 1996
A:Title: Developmental and growth temperature regulation of two different microsc
A:Reference number: Z16095
A:Accession: T07687
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-387 <HEP>
A:Cross-references: EMBL:L43920; NID:g904151; PID:g904152
A:Experimental source: seed
C:Genetics:
A:Gene: FAD2-1
C:Function:
A:Description: involved in production of polyunsaturated lipids; plays a major ro
A:Note: strongly expressed in developing seeds
C:Superfamily: omega-3 fatty acid desaturase

delta-6 fatty acid desaturase (EC 1.14.99.-) - human
 C:Species: Homo sapiens (man)
 C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 13-Aug-1999
 C:Accession: T13155
 R:Cho, H.P.; Nakamura, M.T.; Clarke, S.D.
 J. Biol. Chem. 274, 471-477, 1999
 A:Title: Cloning, expression, and nutritional regulation of the mammalian Delta-6 desaturase
 A:Reference number: 217612; MUID:99085046
 A:Accession: T13155
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-444 <CHO>
 A:Cross-references: EMBL:AF126799; NID:g4406527; PID:g4406528; PIDN:AAD20018.1
 C:Keywords: oxidoreductase

Query Match 15.4%; Score 374.5; DB 2; Length 444;
 Best Local Similarity 26.5%; Pred. No. 3.1e-23;
 Matches 118; Conservative 70; Mismatches 166; Indels 91; Gaps 17;

QY 6 QHEHPEFFIKIDKWCQIDDAVL-----SHPGGS-AITTYKNMDATVFTHTGSK 58
 DB 27 QKHNN---LRTD-RWLVIDRKYNTKWSIQHPGQVRVIGHYAGEDATDAFRAHFDLEFV 82
 QY 59 YQWLT-----ELKKECTQPEIPDKDDPIKIGIDVNMGTENISEKRSQAQINKSFDDL 113
 DB 83 GFLKPLLLIGELAPEPSQD-----HGNKSKITIEDFRALR 117
 QY 114 MRVRAEGLDGSPLFIRKI-----LETI--FTILFAFYQYHTYILP-----SAILMGVAV 163
 DB 118 KTAEDNLFKTNHVFLLAHIALESIAWFTV---FY--FGNGWIPITLITAFVLATSQ 172
 QY 164 QQLGWLHIEFAHQLKRNRYNDLASYVGNFLQGSFGGKQHNHHAATNVVGRDGD 223
 DB 173 AQAGWLQHDYGLHSYVRKPNKNNLVHKEVIGHLKGSANWNNHRRHQHAKPNIFHKDPD 232
 QY 224 LDLVPFYATVAEHLNYSQDSWMTLFRWQHVTMFLPFLRLSWLLQSIFVSOMPTHY 283
 DB 233 VNMHLVFLGEGWQPIEYGGKKLKYLPYNHQHEFFLIGPPLIPMYFOYIIM----- 286
 QY 284 YDYRNTAIYEQVGLSLHAWSGQLYFLPDWSTIRMFVLSHLVGG-----FLLSH 335
 DB 286 -----TMIVHKNNWDLAWAVS---YYIRFFITYIPFY---GILGALLFLNIFRLESH 332
 QY 336 -----VYTFNHYSEKALSSNIMSNYACIQINTRNRPORFTDWLWGLNLYOIEHLLFP 391
 DB 333 WFWVTQMNHIVME---IDQAYRDMFSSQLTATCNVEQSFFNDWFSGLNLFQIEHLLFP 389
 QY 392 TMRPNHNTVMPVLKVEFAAANGLPY 416
 DB 390 TMRPNHNLKIAPLVKSCLKAKHGIEY 414

RESULT 3
 JG0180
 delta-6 fatty acid desaturase (EC 1.14.99.-) - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 13-Aug-1999
 C:Accession: JG0180
 R:Aki, T.; Shimada, Y.; Inagaki, K.; Higashimoto, H.; Kawamoto, S.; Shigeta, S.; Ono, K.
 Biochem. Biophys. Res. Commun. 255, 575-579, 1999
 A:Title: Molecular cloning and functional characterization of rat delta-6 fatty acid desaturase
 A:Reference number: JG0180
 A:Accession: JG0180
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-444 <AKI>
 A:Cross-references: DBJ:AB021980
 C:Superfamily: cytochrome b5 core homology
 C:Keywords: oxidoreductase
 F:18-94/Domain: cytochrome b5 core homology <CB5>

Query Match 15.1%; Score 367; DB 2; Length 444;
 Best Local Similarity 25.1%; Pred. No. 1.3e-22;
 Matches 123; Conservative 64; Mismatches 174; Indels 130; Gaps 17;

QY 4 REQEHEFFIKIDKWCQIDDAVL-----RSHPGG-SAITTYKNMDATVFTHTGSK 56
 DB 22 RWEEIQKHNLRD-RWLVIDRKYNTKWSQHPGGRVIGHYSGEDATDAFRAHFLDLD 80
 QY 57 EAYOWLTAK-KECPTQPEIPDKDDPIKIGIDVNMGTENISEKRSQAQINKSFDTLMR 115
 DB 81 FVGKFLKPLLLIGELAPEP-----SLDRGKSSQITEDFRALKKT 119
 QY 116 VRAEGLDGSPLFYIRKILETITILFAFYL--QYHTYILP-----SAILMGVAVQOGLWLI 170
 DB 120 AEDNLFKTNHVFLLSHIIVNESIAWFTVITVITAFVLATSQAQAGWLQ 179
 QY 171 HEFAHQLKRNRYNDLASYVGNFLQGSFGGKQHNHHAATNVVGRDGDLDLPFY 230
 DB 180 HDYGLHSYVKKSTWNNHVKFVIGHLKGSANWNNHRRHQHAKPNIFHKDPDI----- 234
 QY 231 ATVAEHLNYSQDSWMTLFRWQ-----HVHWTFML---PFLRLSWLLQS 272
 DB 234 -----KSLHVFVLGEGWQPIEYGGKKLKYLPYNHQHEFFLIGPPL----- 275
 QY 273 IIFVSOMPTHYDYRNTAIYEQVGLSLHAWMS-----LGQLYFLPDWST 317
 DB 275 -----IPMYFOYIIMTMRDWDLAWAISYARFFYTYIPFYGILGALVFL----- 324
 QY 318 RIMFFVLVSH-LVGGFLLSHVW---TFNHYSEKALSSNIMSNYACIQIMTTRNMRPGRF 373
 DB 324 NFRFLESHWFWVTQMNHIVMEIDLHY-----RWFSSQLAATCNVEQSFF 371
 QY 374 IDMLWGLNLYOIEHLLFPDMRNHNTVMPVLKVEFAAANGLPYVWDDYFTGFWLEIEQFR 433
 DB 372 NDWFSGLNLFQIEHLLFPDMRNHNLKIAPLVKSCLKAKHGIEYQ-----EKPLLR 421
 QY 434 NIANVAAKLTK 444
 DB 422 ALLDIYSSLKK 432

RESULT 4
 T08765
 probable delta-6 fatty acid desaturase (EC 1.14.99.-) - human (fragment)
 N:Alternate names: protein DKFZp586C201.1
 C:Species: Homo sapiens (man)
 C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 13-Aug-1999
 C:Accession: T08765
 R:Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
 submitted to the Protein Sequence Database, March 1999
 A:Reference number: Z16471
 A:Accession: T08765
 A:Molecule type: mRNA
 A:Residues: 1-311 <WAM>
 A:Cross-references: EMBL:AL050118
 A:Experimental source: adult uterus; clone DKFZp586C201
 C:Genetics:
 A:Note: DKFZp586C201.1
 C:Keywords: oxidoreductase

Query Match 13.0%; Score 316.5; DB 2; Length 311;
 Best Local Similarity 29.0%; Pred. No. 1.1e-18;
 Matches 87; Conservative 51; Mismatches 117; Indels 45; Gaps 10;

QY 134 LETI--FTILFAFYQYHTYILP-----SAILMGVAVQOGLWLIHEFAHQLKRNRYNDLA 188
 DB 10 LESIAWFTV---FY--FGNGWIPITLITAFVLATSQAQAGWLQHDYGLHSYVRKPNKNNLV 64
 QY 189 SYFVGNFLQGSFGGKQHNHHAATNVVGRDGDLDLPFYATVAEHLNYSQDSWMT 248
 DB 65 HKFVIGHLKGSANWNNHRRHQHAKPNIFHKDPDYNMHLFVFLGEGWQPIEYGGKKLKYL 124

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	402.5	16.5	458	2	S68358	hypothetical prote
2	374.5	15.4	444	2	T13155	delta-6 fatty acid
3	367	15.1	444	2	JG0180	delta-6 fatty acid
4	316.5	13.0	311	2	T08765	probable delta-6 f
5	211	8.7	359	2	S35157	Delta(6)-desaturas
6	211	8.7	368	2	S54809	linoleoyl-CoA desa
7	165.5	6.8	387	2	T07687	omega-6 desaturase
8	149.5	6.1	287	2	T11959	fatty-acid desatur
9	144.5	5.9	352	2	B69901	fatty-acid desatur
10	142	5.8	385	2	T09880	omega-6 desaturase
11	140.5	5.8	427	2	G70590	probable desA3 pro
12	139.5	5.7	347	2	S43771	phosphatidylcholin
13	139.5	5.7	383	2	T07688	omega-6 desaturase
14	138	5.7	387	2	T09839	oleate 12'-hydroxyl
15	137	5.6	383	2	T10480	Delta12 Oleate des
16	137	5.6	383	2	T10789	omega-6 desaturase
17	136.5	5.6	359	2	S52650	omega-3 fatty acid
18	131.5	5.4	378	2	T14269	delta-12 oleate de
19	131	5.4	350	2	S43772	phosphatidylcholin
20	129.5	5.3	424	2	JCS891	omega 6 desaturase
21	129	5.3	351	2	S54259	Delta12-desaturase
22	126	5.2	382	2	T15042	omega-6 fatty acid
23	125	5.1	383	2	T15043	fungal elicitor-in
24	124.5	5.1	351	2	S11519	phosphatidylcholin
25	120.5	4.9	443	2	T08136	probable omega-6 d
26	119.5	4.9	447	2	S53309	n-6 fatty acid des
27	114.5	4.7	349	2	S43770	phosphatidylcholin
28	114	4.7	312	2	S77365	hypothetical prote
29	113.5	4.7	369	2	S75038	hypothetical prote
30	111	4.6	659	2	S10228	parasporal crystal
31	108.5	4.5	442	2	S74801	ammonium transport
32	107	4.4	983	2	A59054	chitin synthase (E
33	106	4.4	424	2	T07742	omega-6 desaturase
34	103.5	4.3	652	2	I39811	gene cryIIIB2 prot
35	102.5	4.2	573	2	F70860	probable cytochrom

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Qy 12 FIKIDKWCIODDAVIRSHPGGSA-ITTYKNMDATTVFTHFTGSKAEAWOMTELKKECP.70
   :| |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |
Db 34 WISILKVYVNTWEA-KEHPGGDAPLINLAGODVTDAFIAFHPT-----AW-----80

Qy 71 TQPEIPDIKDPIKIGIDOVNMGTFNISSEKRSQAQINKSFIDLRMVRVAEGLMDGS-----126
   :| |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |
Db 80 -----KHLDKLFTG-YHCKDYQVSDISRDRYKKLASEFAKAGMEFKKGHV1 124

Qy 126 -PLFYRKILET-IFTILF--AFYLQYHTYYLPYSAILMVGVAQQQLGWLLHEFAHHOLFKN 181
   :| |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |
Db 125 YSCLFSVLLLSACVYGVLVSGSWI-----HMLSGAILGLAMQINAYLGHDAGHYQMATT 179

Qy 182 RYXNDLASYPEVGNFLOGFGSGGKKEQHNVHHAATNYVGRGDOLDLVFFYATVAEHUNNVYS 241
   :| |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |
Db 180 GWNKFAGIFIGNCITGISIAWKKWTHNAHHIACNSLDYPDLOHLPLMAVSCKLFNSIT 239

Qy 242 Q-----DSWMFLFRQHVHWTFMPLFFLRSLWSLQSITFV----SOMPHTHYDYDYRN 289
   :| |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |
Db 240 SVEYRGROLTEDPLAREFVSQHYLYYPIMCVARVNLYLOTILLISKRPID-----RG 293

Qy 290 TAIVEQVGLSHAWSLGOLYFLPDWSTRIMEFLVSHLGVGLLSHV-VTENHYSVEKPA 348
   :| |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |
Db 294 LNI-----LGTULIFWTWFLLVSRUWPNPERRVAELVSCFCVTG---IQHIQTLLNHFGSDV- 348

Qy 349 LSSNMSNYACLQIMTTRNNRRCGFIDWLWGGLNYOIEHLLFPTMPRHNLNTVMPLVKEF 408
   :| |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |
Db 348 VGPDKDNWEKOTRTGITDIACSMMWDWFGGLOFOLEHLLPRLPRLCHRLRSISPICREL 407

Qy 409 AAANGLPYMYDDYTGGFWLEIEQOFNRNIANYAAKLT 443
   :| |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |
Db 408 CKYNLPYVSLSVFDVANVTTLKTRTAALQARDLT 442

RESULT 2
T13155

```

RESULT
T13155

RESULT 1

S68358

hypothetical protein - common sunflower

C: Species: *Helianthus annuus* (common sunflower)

C:\projects\newman\images\comment_images
C:\Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999

C;Accession: 568358

R: Sperling, P.; Schmidt, H.; Heinz, E.

Eur. J. Biochem. 232, 798-805, 1995

Exp. 9: Biochem: 232/ 750 005/ 1333
A:Title: A cytochrome-b(5)-containing fus

A-Reference number: S68358: MUID: 96028121
A-Title: A CYCLOTRON BEAM CONFINING LASER

A: Release number: 568358

A; ACCESSION: 508350
A; STATUS: preliminary

A: status: preliminary
A: Molecule type: tRNA

A;Molecule type: mRNA
A:Pos:1406: 1-158 /CDEF

A;Residues: I-438 <SPE>
 A:GCGCGCTGCGCGCGCG: EMPI:Y97113: NID:G1040728: PID:G1040729

A; Cross-references: EMBL:X87143; NIB:gl040

C;Superfamily: cytochrome b5 core homology

F;16-90/Domain: cytochrome b5 core homology <CB5>

```
Query Match
16.5%: Score 402.5; DB 2; Length 458;
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Best Local Similarity	24.8%;	Pred. No. 1.6e-25;
Matches 113:	Conservative	89: Mismatches 184;
		Indels 69: Gaps 16;

[illegible]

RESULT
T13155

NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/337,483
FILING DATE: 08-NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-410 MIS:jb
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 107:
SEQUENCE CHARACTERISTICS:
LENGTH: 911 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-337-483-107

Query Match 10.0%; Score 243.448; DB 2; Length 911;
Best Local Similarity 27.6%; Pred. No. 6.6e-16;
Matches 21; Conservative 7; Mismatches 26; Indels 22; Gaps 5;
Qy 172 EFAPHQLFKRYNDLASVFGNFIQGFSSGGWKEQ-----HNVHHAATNVVGRDGLDL 226
Db 691 EISH---FSNAYRNLIA-----FAEELSKNGTTGKNGYGHNAQNAKLGVNITAQDLDF 741
Qy 227 -----VFF--YATVA 234
Db 742 NGLMKRIPYGYATFA 757

RESULT 15
5223423-2
Patent No. 5223423
APPLICANT: FRANCHINI, GENOVEFFA; WONG-STAAL, FLOSSIE;
GALLO, ROBERT
TITLE OF INVENTION: CHARACTERIZATION OF REPLICATION COMPETENT
HUMAN IMMUNODEFICIENCY TYPE 2 PROVIRAL CLONE HIV-2 SBL/ISY
NUMBER OF SEQUENCES: 4
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/331,212
FILING DATE: 03-31-1989
SEQ ID NO: 2
LENGTH: 3077
5223423-2

Query Match 9.8%; Score 238.092; DB 5; Length 3077;
Best Local Similarity 19.8%; Pred. No. 1.3e-14;
Matches 33; Conservative 24; Mismatches 46; Indels 64; Gaps 11;
Qy 204 WKE-QHNVHHAATNVVGRDGLDLVPFYATVAEHLNNYSQDSWVMTLFRWQ-HVHWTFML 261
Db 2548 WQWEHKIRFLEANI---SESLE-----QAQIQEKNMVE---LQKLSNWDVFGNW---- 2593
Qy 262 PFLRLSWL-----LQSIIFVSQMPHYDYRYNTAI-----Y 293
Db 2593 -FDUTSWIKYIQYGMVIVGIVALRVIVYVQMLSLRLKRGYRPVSLPPGYIQQIHKDW 2651

Qy 294 EQ-----VGLSLHWAWSLGQLYFLPDKSTRIMFTLVSHL 327
Db 2652 EQPDREETEEDVNDVG-SRSWPPFIYIHFL-----IRLLIRLLTRL 2693
Search completed: February 25, 2000, 00:29:31
Job time: 25089 sec

RESULT 12

US-08-337-483-5

; Sequence 5, Application US/08337483

; Patent No. 5922562

; GENERAL INFORMATION:

; APPLICANT: Loosmore, Sheena

; APPLICANT: Harkness, Robin

; APPLICANT: Schryvers, Anthony

; APPLICANT: Chong, Pele

; APPLICANT: Gray-Owen, Scott

; APPLICANT: Yang, Yan-Ping

; APPLICANT: Murdin, Andrew

; APPLICANT: Klein, Michel

; TITLE OF INVENTION: Transferrin Receptor Genes

; NUMBER OF SEQUENCES: 147

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Sim & McBurney

; STREET: Suite 701, 330 University Avenue

; CITY: Toronto

; STATE: Ontario

; COUNTRY: Canada

; ZIP: M5G 1R7

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/337,483

; FILING DATE: 08-NOV-1994

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Stewart, Michael I

; REGISTRATION NUMBER: 24,973

; REFERENCE/DOCKET NUMBER: 1038-410 MIS:jb

; TELEPHONE: (416) 595-1155

; TELEFAX: (416) 595-1163

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 913 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; US-08-337-483-5

Query Match

Best Local Similarity 24.1%; Score 243.52; DB 2; Length 913;

Matches 28; Conservative 20; Mismatches 45; Indels 23; Gaps 7;

Qy 375 SHLVGGFLLSHVTFNHYSVKFAALSSNMSYACIQIMTTRMRPGFIDWLWGLNLYQ 384

Db 550 AELVGGDLNCGKSSNSDCKVRLKG--KNY---YFAARNMALGKIVD-LGLGMRYD 603

Qy 385 IEHHLFTPMRRLNTV-MPLVKEFAAANGLPYVDDYFTGFWEIEQ-----FRN 434

Db 604 V-----SRTKANESTISVGKFNFSWNTGIVIKTE-----WLDLSYRLSTGFRN 648

RESULT 13

US-08-478-435-107

; Sequence 107, Application US/08478435

; Patent No. 5922323

; GENERAL INFORMATION:

; APPLICANT: Loosmore, Sheena

; APPLICANT: Harkness, Robin

; APPLICANT: Schryvers, Anthony

; APPLICANT: Chong, Pele

; APPLICANT: Gray-Owen, Scott

; APPLICANT: Yang, Yan-Ping

; APPLICANT: Murdin, Andrew

; APPLICANT: Klein, Michel

; TITLE OF INVENTION: Transferrin Receptor Genes

; NUMBER OF SEQUENCES: 147

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Sim & McBurney

; STREET: Suite 701, 330 University Avenue

; CITY: Toronto

; STATE: Ontario

; COUNTRY: Canada

; ZIP: M5G 1R7

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/478,435

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/337,483

; FILING DATE: 08-NOV-1994

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/175,116

; FILING DATE: 29-DEC-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/148,968

; FILING DATE: 08-NOV-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Stewart, Michael I

; REGISTRATION NUMBER: 24,973

; REFERENCE/DOCKET NUMBER: 1038-462 MIS:vg

; TELEPHONE: (416) 595-1155

; TELEFAX: (416) 595-1163

; INFORMATION FOR SEQ ID NO: 107:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 911 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; US-08-478-435-107

Query Match 10.0%; Score 243.448; DB 2; Length 911;

Best Local Similarity 27.6%; Pred. No. 6.6e-16;

Matches 21; Conservative 7; Mismatches 26; Indels 22; Gaps 5;

Qy 172 EFAHQHQLFKNRYNDLASYFVGNFLQGFSSGGWKQ-----HNVHAATNYYVGRGDDL 226

Db 691 EISH---FSNAYRNLIJA-----FAEELSKNGTGTGKNGYHNAQNAKLVGVNITAQLDF 741

Qy 227 -----VVF--YATVA 234

Db 742 NGLWKRIPIGWYATFA 757

RESULT 14

US-08-337-483-107

; Sequence 107, Application US/08337483

; Patent No. 5922562

; GENERAL INFORMATION:

; APPLICANT: Loosmore, Sheena

; APPLICANT: Harkness, Robin

; APPLICANT: Schryvers, Anthony

; APPLICANT: Chong, Pele

; APPLICANT: Gray-Owen, Scott

; APPLICANT: Yang, Yan-Ping

; APPLICANT: Murdin, Andrew

; APPLICANT: Klein, Michel

; TITLE OF INVENTION: Transferrin Receptor Genes

5187091-2
LENGTH: 652

Query Match 10.4%; Score 253.184; DB 5; Length 652;
Best Local Similarity 18.1%; Pred. No. 4.3e-17;
Matches 98; Conservative 68; Mismatches 190; Indels 185; Gaps 22;

QY 31 PGSSAIIYKNDATTVEHFFHGSKEAYOW-----LTELKKECPQPEIPDIK- 81
DB 83 PRGALTSYFOSLNTIW-----PSDADPWKAFMAQVEVLIDKKIEEYAKSKALAELOQ 136
QY 81 -----DDPIKIGDDVNGFTNISEKSA-QINKSFIDLRMRVRAEGLMDGSPFLYIRKIL 134
DB 137 LQNNFEDYVNALNSWKKTPLSLRSKRSQDRIRLFQAESHFR-----NSMPSFAVSK-F 190
QY 135 ERIFTILFAYLOYHTYIYPSAILMGVAMQOLGWLHFEFAHOLFKNRYND--LASIFY 192
DB 191 EYLFPTYAAANTHLLLLKDAQVFGGEWGYSSDVAEFYHROLKLTQYTDHCVNWNV 250
QY 193 G-NFQGSSEGGKQOHNVHAATNVGRDGLDLV---PFYATVAEHLNNYSQDSWVMT 248
DB 251 GUNGLRGSTYDAWVFNFRREMTLV-----LDLVLFPFY-----DIRLSKG----- 296
QY 249 LFRQHVHWTMLPFLRLSLW-----LQSIIFVSOMPHY--- 284
DB 296 -VKTELTRDIFDPIFSLATLOEYGTFLSIENSIRKPHLDYLOGIEFTRLQPGYFK 354
QY 284 -DYIRNT-----AIYEQVGLSLHWASL 306
DB 355 DSFNWGSNGYVETRPISGSKTITSPFYGDKSTEPYQKLSFDGQKVRTIANTDVAAPN 414
QY 307 GOLYFLPDWSTRIMFLVSHLVGGFLLSHVTFNHYSVKEFALSSNIMS----- 356
DB 415 GRVY-----LGVTKYDFSQDDQKNTSTQTYDSKRNNHVSQAQ 453
QY 356 -----NYA-CLQIMTTRNMRPGRFIDWLWGLNLYOIEHHLFP 391
DB 454 DSIDQLPPTTDEPLEKAYSHQNLNAECFLMODRRGTIP--FTWTHRSVDF-----FN 505
QY 392 TMRNRLNLTVPYKFEFAANGLPMVDDYFTGFWL-----EIOFRNTANVAAKLT 443
DB 506 TIDAEKI-TOLPVKRAYALSSGASIEGPGFTGNNLLFKESSNIAKFKVTLNSAALLQ 564
QY 444 K 444
DB 565 R 565

5223423-4
LENGTH: 3080

Query Match 10.4%; Score 253.124; DB 5; Length 3080;
Best Local Similarity 22.4%; Pred. No. 4.1e-16;
Matches 15; Conservative 14; Mismatches 23; Indels 15; Gaps 3;
QY 271 QSIIFVSOMPHYDYRYNTAIYEQVGLSLHWANSLGOLYFLPDWS-----TRIMEFL 323
DB 1143 EALVINGRIPKFLHLPVERET--WEO-----WMDNVQVWTIPDWDVFTPLVRLAFNL 1194

QY 324 VSHLVGG 330
DB 1195 VKDPIPG 1201

RESULT 11

US-08-478-435-5
Sequence 5, Application US/08478435
Patent No. 5922323
GENERAL INFORMATION:
APPLICANT: Loosmore, Sheena
APPLICANT: Harkness, Robin
APPLICANT: Schryvers, Anthony
APPLICANT: Chong, Pele
APPLICANT: Gray-Owen, Scott
APPLICANT: Yang, Yan-Ping
APPLICANT: Murdin, Andrew
APPLICANT: Klein, Michel
TITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
ADDRESS: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478.435
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/337,483
FILING DATE: 08-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/148,968
FILING DATE: 08-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-462 MIS:vg
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 913 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-478-435-5

Query Match 10.0%; Score 243.52; DB 2; Length 913;
Best Local Similarity 24.1%; Pred. No. 6.5e-16;
Matches 28; Conservative 20; Mismatches 45; Indels 23; Gaps 7;
QY 325 SHLVGGFLLSHVTFNHYSVKEFALSSNINMNACTIOTRNNRPRFIDWLWGLNLYQ 384
DB 550 AELVGGDLCKQKSSNICKVRLKIG--KNY---YFAARNNALGKYVD-LGLGMYD 603
QY 385 IEHLFTMPRHLNLTVMPLVKFAAANGLPYMVDDYFTGFWLEIQ-----FRN 434
DB 604 V-----SRKANEISISVCKFKFNFSWNTGIVIKPTE-----WLDLSYRLSTGFRN 648

```

; TITLE OF INVENTION:  OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANT
; NUMBER OF SEQUENCES:    18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
; STREET:   260 SHERIDAN AVENUE, P.O. BOX 60039
; CITY:     PALO ALTO
; STATE:    CA
; COUNTRY:  USA
; ZIP:      94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834.655
; FILING DATE: 11-APR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: RAE-VENTER, BARBARA
; REGISTRATION NUMBER: 32,750
; REFERENCE/DOCKET NUMBER: CGNE.124.00US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 328-4400
; TELEFAX: (650) 328-4477
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 252 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-834-655-7

Query Match          10.7%; Score 259.5; DB 2; Length 252;
Best Local Similarity 25.5%; Pred. No. 2.5e+18;
Matches 63; Conservative 49; Mismatches 110; Indels 25; Gaps 6

Qy 155 SAILMGVAWQQGLWLHFEFAHHOLFKNRYVNDLASFYFGNVLQGFSGGGKOEHNHVHAA 214
Db 18 AALGLLWTQSIVIGHDSGHVIMSNKSYNRFAGLLSGNCUTGISIAWKWTHNAHLA 77
Qy 215 TNYVGROGDLDLPFFATVAEHLNNYSQDSW-----VMTLFRWQHVVHTMPLFLR 265
Db 78 CNSLDYPDLOHIPVFAYSTAFFESSLTSEFYDRKLTFGPVARFELSYQHFTYYPVNCFGR 137
Qy 266 LSWLQSIIFY--SQMPHYDYIRNTAIYEQVGLSLHWAVSNGOLYFLPDWSKTRIMEFF 322
Db 138 INFLEIQTFLLLFSKREVPDRALNF-----AGILVEVTWFPLLVSCLPNWPERRFFV 188
Qy 323 LVSHLVGGFLLSHV-VFNHNHSVEKEAFSSNMISNVACLOINTNRMRPGRITDLWGGL 381
Db 189 FTSETVTA--LQHIQFTLNHFADVI-YGPPTGSDWFEEKQAAGTIDISCRSYDNDFEGGL 245
Qy 382 NYQIEHH 388
Db 246 QFQLEHH 252

RESULT 9
5187091-2
; Patent No. 5187091
; APPLICANT: DONOVAN, WILLIAM P.; RUPAR, MARK J.; SLANEY, ANNETTE C.; JOHNSON, TIMOTHY B.
; TITLE OF INVENTION: BAGILLUS THURINGIENSIS CRYPTIC GENE . ENCODING TOXIC TO COLEOPTeran INSECTS
; NUMBER OF SEQUENCES: 2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/496.568
; FILING DATE: 20-MAR-1990
; SEQ ID NO:2
```

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/366,779
 FILING DATE: 30-DEC-1994
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: Presser, Leopold
 REGISTRATION NUMBER: 19,827
 REFERENCE/DOCKET NUMBER: 83832YXW
 TELEPHONE: (516) 742-4343
 TELEFAX: (516) 742-4366
 TELEX: 230 901 SANS UR
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 448 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-366-779-5

Query Match 16.6%; Score 403.5; DB 1; Length 448;
 Best Local Similarity 27.0%; Pred. No. 2.1e-32;
 Matches 123; Conservative 69; Mismatches 199; Indels 65; Gaps 16;

QY 12 FIKDQKWCDDAVLRSHPGGS-AITTYKNMDATTVFHTGSKAYQHLTELKKECP 70
 DB 24 WISQRAYDVSDWV-KDHPGSGPLKSLAGQEVTDFAVAFHPAS-----TW----- 70
 QY 71 TOPEIPDKDDPIKIDDDVNMGTFNISERSAQINKSFTDLRMVRAEGLMDG----- 125
 DB 70 -----KNLDKFFTG-YILKDYSEVSKDYRKLVFEFSKMGLYDKKHIMF 114
 QY 125 SPLFYIRKILE-TIFTLFAFYQYHTYIPLSAILMGVAMQQLGWLIEFAHQLKKNRY 183
 DB 115 ATLCFIAMLFAMSVYGLFCEGLVHLF---SGCLMGFLWISQWIGHDAGHYVWVSDSR 171
 QY 184 YNDLASVFNGLQSGSGGKQEHNVHHAATNVVGRDGLDLP-----FYATVAEH 236
 DB 172 LNFEMGIFAANCLSGISIGWKNWNAHHAACNSLEYDPPDQYIPFLVSSKFFGSLTS 231
 QY 237 L--NNYSQDSVMWTLFRQVHWTFF--MLPFLRLSLLQSIIFVSQMPHYDYRNTA- 292
 DB 232 FYEKRLTFDS--LSRFFVSQHWTFYIPMCAARLNNYVQSLIMLLTK-----RVNSY 281
 QY 292 -IYEQVGLSHWANSGLQLYFLPDWSTRIMFFLVSHLVGGLLHVVTNNHYSVEKFA 350
 DB 282 RAQELGLCLVFSIWYPLLVSCPLNMGRIIMFVIAASLVGTG-MQOVQFSLNHFSVY-VG 339
 QY 351 SNIMSNYACLOIQTTRNMRPGRFIDWGLNQLVQIEHHLFPTMPRHNLNTVMPVKEFAA 410
 DB 340 KPGKNWFEKQTDGTDLDISCPMPWDFHGGSGQFQIEHHLFPKMPRCNLRKISPYIELCK 399
 QY 411 ANGLPYMVDYFTGFWELEIQFRNIANVAALKTKKI 446
 DB 400 KHNLPYNASFSKANEMTLTLNTALQARDITKPL 435

RESULT 6

US-08-789-936-5
 Sequence 5, Application US/08789936
 Patent No. 5789220

GENERAL INFORMATION:

APPLICANT: Thomas, Terry L.
 APPLICANT: Reddy, Avutu S.
 APPLICANT: Nuccio, Michael
 APPLICANT: Freyssinet, Georges L.
 APPLICANT: Nunberg, Andrew N.
 TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A

TITLE OF INVENTION: DELTA 6-DESATURASE
 NUMBER OF SEQUENCES: 25
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Scully, Scott, Murphy & Presser
 STREET: 400 Garden City Plaza
 CITY: Garden City
 STATE: New York
 COUNTRY: United States
 ZIP: 11530
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/789,936
 FILING DATE: 28-JAN-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/366,779
 FILING DATE: 30-DEC-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Presser, Leopold
 REGISTRATION NUMBER: 19,827
 REFERENCE/DOCKET NUMBER: 83832YXW
 TELEPHONE: (516) 742-4343
 TELEFAX: (516) 742-4366
 TELEX: 230 901 SANS UR
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 448 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE:
 US-08-789-936-5

Query Match 16.6%; Score 403.5; DB 1; Length 448;
 Best Local Similarity 27.0%; Pred. No. 2.1e-32;
 Matches 123; Conservative 69; Mismatches 199; Indels 65; Gaps 16;

QY 12 FIKDQKWCDDAVLRSHPGGS-AITTYKNMDATTVFHTGSKAYQHLTELKKECP 70
 DB 24 WISQRAYDVSDWV-KDHPGSGPLKSLAGQEVTDFAVAFHPAS-----TW----- 70
 QY 71 TOPEIPDKDDPIKIDDDVNMGTFNISERSAQINKSFTDLRMVRAEGLMDG----- 125
 DB 70 -----KNLDKFFTG-YILKDYSEVSKDYRKLVFEFSKMGLYDKKHIMF 114
 QY 125 SPLFYIRKILE-TIFTLFAFYQYHTYIPLSAILMGVAMQQLGWLIEFAHQLKKNRY 183
 DB 115 ATLCFIAMLFAMSVYGLFCEGLVHLF---SGCLMGFLWISQWIGHDAGHYVWVSDSR 171
 QY 184 YNDLASVFNGLQSGSGGKQEHNVHHAATNVVGRDGLDLP-----FYATVAEH 236
 DB 172 LNFEMGIFAANCLSGISIGWKNWNAHHAACNSLEYDPPDQYIPFLVSSKFFGSLTS 231
 QY 237 L--NNYSQDSVMWTLFRQVHWTFF--MLPFLRLSLLQSIIFVSQMPHYDYRNTA- 292
 DB 232 FYEKRLTFDS--LSRFFVSQHWTFYIPMCAARLNNYVQSLIMLLTK-----RVNSY 281
 QY 292 -IYEQVGLSHWANSGLQLYFLPDWSTRIMFFLVSHLVGGLLHVVTNNHYSVEKFA 350
 DB 282 RAQELGLCLVFSIWYPLLVSCPLNMGRIIMFVIAASLVGTG-MQOVQFSLNHFSVY-VG 339
 QY 351 SNIMSNYACLOIQTTRNMRPGRFIDWGLNQLVQIEHHLFPTMPRHNLNTVMPVKEFAA 410
 DB 340 KPGKNWFEKQTDGTDLDISCPMPWDFHGGSGQFQIEHHLFPKMPRCNLRKISPYIELCK 399
 QY 411 ANGLPYMVDYFTGFWELEIQFRNIANVAALKTKKI 446
 DB 400 KHNLPYNASFSKANEMTLTLNTALQARDITKPL 435

TELEFAX: (650) 328-4477
 TELEX: N/A
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 355 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-834-655-5

Query Match 22.88; Score 555; DB 2; Length 355;

Best Local Similarity 34.58; Pred. No. 9.8e-48;
 Matches 124; Conservative 65; Mismatches 134; Indels 36; Gaps 8;

QY 112 LRMVRAEGLMDGSPLEFIRKI-----LETITLILFAYLYQHY-YLPSSAILMGVAMQ 165
 DB 5 LRTLFQSLGYDSSKAYAFKVSFNLGSLTVIVAKWGOTSTLANVLSAALLGLFWQ 64
 QY 166 LGWLIHEFAHQFKNRYNDLASYFVGNFLOGFSSGGWKEQHNHHAATNVVGRDGLD 225
 DB 65 CGWLADFLHQVDFQDFWGLDGLFAGLVGVCQGFSSWKKHNTTHAAPNVHGEDPDID 124
 QY 226 LVFAYATVAHLNYSOD-----SWMTLFRQHVHTF--MLPELRLSLWLLQSIIFV- 277
 DB 125 THPL-LTWSEHALEMFSDVDELTRMWSRFWLNQTFYPPILSFARLSWCLQSILFVL 183
 QY 277 -----SOMPTHYDYRNTAIYEQVGLSLHAWSLGQLY-FLPDWSTRIMEFLVS 325
 DB 184 PNGAHPKSPGARVP-----ISLVEQLSLAMHTWYLATMFLFKDPNMLVYFLVS 234
 QY 326 HLVGGLLSHYVTNHYNSVEKFAESSNIMSNYACLIQMTTRNMRPGRFIDMLWGLNLYQI 385
 DB 235 QAVCGNLLAIVSLNHNMGMPVISKEEAVDMDFETKQITGRDVHPGLFANFTGLNLYQI 294
 QY 386 EHLFPTMPRHNLNTVPLVKEFAAAGLPMVDDYFTGFWELEIQFNRNIANVAKLTK 444
 DB 295 EHLFSPMRHNFSKIOPAVETLCKKNYRHTTGMIEGTAEVFSRLNEVSKAAMKMK 353

RESULT 4

US-08-833-610-5
 ; Sequence 5, Application US/08833610
 ; Patent No. 5972664
 ; GENERAL INFORMATION:
 ; APPLICANT: KNUTZON, DEBORAH
 ; APPLICANT: MURKERJI, PRADIP
 ; APPLICANT: HUANG, YUNG-SHENG
 ; APPLICANT: THURMOND, JENNIFER
 ; APPLICANT: CHAUDHARY, SONITA
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
 ; OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
 ; STREET: 260 SHERIDAN AVE, P.O. BOX 60039
 ; CITY: PALO ALTO
 ; STATE: CALIFORNIA
 ; COUNTRY: USA
 ; ZIP: 94306
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/833.610
 ; FILING DATE: 11-APR-1997
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: RAE-VENTER, BARBARA
 ; REGISTRATION NUMBER: 32,750

REFERENCE/DOCKET NUMBER: CGNE.123.00US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650)328-4400
 TELEFAX: (650)328-4477
 TELEX: N/A
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 446 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-833-610-5

Query Match 16.74; Score 407.5; DB 2; Length 446;
 Best Local Similarity 27.24; Pred. No. 8.3e-33;
 Matches 124; Conservative 69; Mismatches 198; Indels 65; Gaps 16;

QY 12 FIKDGGKWCQIDDAVLRSHPGGS-AITYKNMDATTVFHTFTGSKAYOMLTCLKKECP 70
 DB 24 WISIOGRAYDVSDWV-KDHPGGSPLKSLAGQVTDFAVAFHPS-----TW----- 70
 QY 71 TQPEIPIKDDPIKIGIDDDVNMGTENISEKRSQAQINKSFTDLRMVRAEGLMDG----- 125
 DB 70 -----KNLDKFTG-YLKDYSVSEVSKYKLVFEFSKMGLYDKKGHMF 114
 QY 125 SPLPYIRKILE-TITLILFAYLYQHYIYLPSSAILMGVAMQOOLGWLIIHEFAHQFKNRY 183
 DB 115 ATLCFIAMLFAMSYGVGLFCEGLVHLF---SGCLMGFLWIOSGIGHDAGHYMVVSDSR 171
 QY 184 YNDIASFVGNFLOGFSSGGWKEQHNHHAATNVVGRDGLDLP-----FYATVAEH 236
 DB 172 LNKFMGIFAACNLGSIIGWKNHNAHTACNSLEVDYDQYIPFLVSSKFGSLTSH 231
 QY 237 L--NNYSQDSWMTLFRQHVHTF--MLPELRLSLWLLQSIIFYSQMPTHYDYRNTA- 292
 DB 232 FYEKLRFDS--LSRFVSYQHWTFYIPMCAARLNMVQSLIMLLTK-----RNVSY 281
 QY 292 -IYQVGLSLHAWSLGQLYFLPDWSTRIMEFLVSHLVGGFLLSHVVTFNHYNSVEKFA 350
 DB 282 RAQELGLCLVFSIWYPLLVSLCPNKGRIEVIASLVG-MQOVQFSLNHFSSVY-VG 339
 QY 351 SNIMSNYACLIQMTTRNMRPGRFIDMLWGLNLYQIEHLLFPTMPRHNLNTVPLVKEFAA 410
 DB 340 KPGNNWFKEQTDGTDLDISCPWMDWFGGLQFQIEHLLFPTMPRCNLRKISPYVIELCK 399
 QY 411 ANGLPMVDDYFTGFWELEIQFNRNIANVAKLTKKI 446
 DB 400 KHNLPYVASFPSKANWTLRLTNALQARDITKPL 435

RESULT 5

US-08-366-779-5
 ; Sequence 5, Application US/08366779
 ; Patent No. 5614393
 ; GENERAL INFORMATION:
 ; APPLICANT: Thomas, Terry L.
 ; APPLICANT: Reddy, Avutu S.
 ; APPLICANT: Nuccio, Michael
 ; APPLICANT: Freccinet, Georges L.
 ; APPLICANT: Nundberg, Andrew N.
 ; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Scully, Scott, Murphy & Presser
 ; STREET: 400 Garden City Plaza
 ; CITY: Garden City
 ; STATE: New York
 ; COUNTRY: United States
 ; ZIP: 11530
 ; COMPUTER READABLE FORM:

Db 80 LANFYVGDIDSDRDIKNDDF-----AAEVRK-----LRTLFQSLGYD 118
Qy 124 GSPFLFYIRKI-----LETIFTILFAFYQVHTY-YLPSAILMGVANOQGLWLIHEFAHQ 177
Db 119 SSKAYAFKVSFNLCTWGLSTVIAKWTSTLANVLSAALLGLFWOQCGWLAHDFLHQ 178
Qy 178 LFKNRYNDLASYFVGNFLOGSSGKKEQHNHHAATNVVGRDGLDLPVFPYATVAEHL 237
Db 179 VFQDRFWGLFGAFLGVCQGFSSSWKDKHNTTHAHPNVHGEDPIDTHPL-LTWSEHA 237
Qy 238 NNYSD-----SWMTLFRQHVHTF--MLPFLRLSWLQSIIFV-----SQ 278
Db 238 LEMFSDVPDEELTRMWSRFVNLQTFYFPLSFARLSWCLOSIILFVLPNGOAHKPSGAR 297
Qy 279 MPTHYDYRNTAIYEQVGLSLHNAWSLGOLY-FLPDWSTRTMFFLVSHLVGGFLLSHVY 337
Db 298 VP-----ISLVEQLSLAMHTWYLATMFLFKDPVNMVLYFLVSOAVCGNLLAIVF 348
Qy 338 TFNHYVSEKFASSNIMSACLOIMTTRNMRPGRFIDWLWGLNLYQIEHHLFPTMPRHN 397
Db 349 SLNHNGMPVISKEEAVIDMDFTKQITGRDVHPGLFANWFTGGLNYQIEHHLFPPSMPRHN 408
Qy 398 LNTVMPLYKEFAAANGLPYVDDYFTGFWLEIEQFRNIANVAALKTK 444
Db 409 FSKIOPAVETLCKKYNRYHTTGMIEGTAEVFSRLNEVSKAASKMGK 455

RESULT 2

US-08-833-610-4
; Sequence 4, Application US/08833610
; Patent No. 5972664
; GENERAL INFORMATION:
; APPLICANT: KNUTZON, DEBORAH
; APPLICANT: MURKERJI, PRADIP
; APPLICANT: HUANG, YUNG-SHENG
; APPLICANT: THURMOND, JENNIFER
; APPLICANT: CHAUDHARY, SUNITA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
; OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
; STREET: 260 SHERIDAN AVE, P.O. BOX 60039
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833,610
; FILING DATE: 11-APR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: RAE-VENTER, BARBARA
; REGISTRATION NUMBER: 32,750
; REFERENCE/DOCKET NUMBER: CGNE.123.000S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)328-4400
; TELEFAX: (650)328-4477
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 457 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-833-610-4

Query Match 25.5%; Score 620; DB 2; Length 457;
Best Local Similarity 32.8%; Pred. No. 4.3e-54;
Matches 153; Conservative 76; Mismatches 176; Indels 62; Gaps 13;
Qy 4 REQHEPEFFIKIDGKCQIDDAVLASHPGGSAITTKNNKDATVYFTFHTGSKAEQWLT 63
Db 25 KDAEAPFUMIIDNKVYDVREEV-PDHPGGSVILTHVGKDGTDVDFTH---PEA-AWET 79
Qy 64 ELKKECPTPEIPDIKDDPIKIDVNVNGTENISEKRSQAQINKSFDTLRLMRVRAEGLMD 123
Db 80 LANFYVGDIDSDRDIKNDDF-----AAEVRK-----LRTLFQSLGYD 118
Qy 124 GSPFLFYIRKI-----LETIFTILFAFYQVHTY-YLPSAILMGVANOQGLWLIHEFAHQ 177
Db 119 SSKAYAFKVSFNLCTWGLSTVIAKWTSTLANVLSAALLGLFWOQCGWLAHDFLHQ 178
Qy 178 LFKNRYNDLASYFVGNFLOGSSGKKEQHNHHAATNVVGRDGLDLPVFPYATVAEHL 237
Db 179 VFQDRFWGLFGAFLGVCQGFSSSWKDKHNTTHAHPNVHVEDPIDTHPL-LTWSEHA 237
Qy 238 NNYSD-----SWMTLFRQHVHTF--MLPFLRLSWLQSIIFV-----SQ 278
Db 238 LEMFSDVPDEELTRMWSRFVNLQTFYFPLSFARLSWCLOSIILFVLPNGOAHKPSGAR 297
Qy 279 MPTHYDYRNTAIYEQVGLSLHNAWSLGOLY-FLPDWSTRTMFFLVSHLVGGFLLSHVY 337
Db 298 VP-----ISLVEQLSLAMHTWYLATMFLFKDPVNMVLYFLVSOAVCGNLLAIVF 348
Qy 338 TFNHYVSEKFASSNIMSACLOIMTTRNMRPGRFIDWLWGLNLYQIEHHLFPTMPRHN 397
Db 349 SLNHNGMPVISKEEAVIDMDFTKQITGRDVHPGLFANWFTGGLNYQIEHHLFPPSMPRHN 408
Qy 398 LNTVMPLYKEFAAANGLPYVDDYFTGFWLEIEQFRNIANVAALKTK 444
Db 409 FSKIOPAVETLCKKYNRYHTTGMIEGTAEVFSRLNEVSKAASKMGK 455

RESULT 3

US-08-834-655-5
; Sequence 5, Application US/08834655
; Patent No. 5968809
; GENERAL INFORMATION:
; APPLICANT: KNUTZON, DEBORAH
; APPLICANT: MURKERJI, PRADIP
; APPLICANT: HUANG, YUNG-SHENG
; APPLICANT: THURMOND, JENNIFER
; APPLICANT: CHAUDHARY, SUNITA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
; OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
; STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,655
; FILING DATE: 11-APR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: RAE-VENTER, BARBARA
; REGISTRATION NUMBER: 32,750
; REFERENCE/DOCKET NUMBER: CGNE.124.000S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 328-4400

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OM protein - protein search, using sw model

Run on: February 24, 2000, 17:31:22 ; Search time 16.6 Seconds
(without alignments)
358.072 Million cell updates/sec

Title: PCT-US99-28655-2

Perfect score: 2435

Sequence: 1 MVLREQEHEFFIKDKWC.....EIQFRNIANVAALKTKIA 447

Scoring table: BLOSUM62

Searched: 133990 seqs, 13297546 residues

Database : Issued_Patents_AA.*

Word size : 0

Number of hits that pass the threshold : 133990
1: /cgn2_6/ptodata/2/iaa/5A.COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B.COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6.COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/PGTUS9.COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	629	25.8	457	2	US-08-834-655-2
2	620	25.5	457	2	US-08-833-610-4
3	555	22.8	355	2	US-08-834-655-5
4	407.5	16.7	446	2	US-08-833-610-5
5	403.5	16.6	448	1	US-08-366-779-5
6	403.5	16.6	448	1	US-08-789-936-5
7	284.5	11.7	87	2	US-08-834-655-10
8	259.5	10.7	252	2	US-08-834-655-7
9	253.184	10.4	652	5	5187091-2
10	253.124	10.4	3080	5	523423-4
11	243.52	10.0	913	2	US-08-478-435-5
12	243.52	10.0	913	2	US-08-337-483-5
13	243.448	10.0	911	2	US-08-478-435-107
14	243.448	10.0	911	2	US-08-337-483-107
15	238.092	9.8	3077	5	523423-2
16	237.02	9.7	1648	2	US-08-662-227-35
17	232.872	9.6	1365	5	5194600-4
18	231.368	9.5	914	2	US-08-478-435-11
19	231.368	9.5	914	2	US-08-337-483-11
20	230.5	9.5	446	2	US-08-833-610-2
21	229.12	9.4	1165	5	5188960-4
22	227.388	9.3	1280	5	5206352-4
23	227.352	9.3	1286	5	5206163-1
24	227.096	9.3	1333	2	US-08-662-227-34
25	227.012	9.3	1642	2	US-08-662-227-2
26	226.248	9.3	2615	5	5206163-3
27	224.592	9.2	912	2	US-08-478-435-7
28	224.592	9.2	912	2	US-08-478-435-9
29	224.592	9.2	912	2	US-08-337-483-7
30	224.592	9.2	912	2	US-08-337-483-9
31	222.212	9.1	1179	5	5188960-2
32	222.584	9.1	845	5	5196194-17
33	218.416	9.0	3025	5	523423-3
34	214.312	8.8	1174	5	5188960-8

35 214.092 8.8 1189 5 5188960-6
36 214.032 8.8 2894 2 US-08-391-671A-23
37 213.268 8.8 919 2 US-08-788-674-4
38 212.772 8.7 751 5 5220013-2
39 212.168 8.7 908 2 US-08-478-435-94
40 212.168 8.7 908 2 US-08-337-483-94
41 211.072 8.7 952 2 US-08-788-674-5
42 211.211 8.7 359 1 US-08-307-382-2
43 211 8.7 359 1 US-08-366-779-2
44 211 8.7 359 1 US-08-478-727-2
45 211 8.7 359 1 US-08-473-508-2

ALIGNMENTS

RESULT 1
US-08-834-655-2
; Sequence 2, Application US/08834655
; Patent No. 5958809
; GENERAL INFORMATION:
; APPLICANT: KNUTZON, DEBORAH
; APPLICANT: MURKERJI, PRADIP
; APPLICANT: HUANG, YUNG-SHENG
; APPLICANT: THURMOND, JENNIFER
; APPLICANT: CHAUDHARY, SUNITA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
; TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
; STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,655
; FILING DATE: 11-APR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: RAE-VENTER, BARBARA
; REGISTRATION NUMBER: 32,750
; REFERENCE/DOCKET NUMBER: CGNE.124.00US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 328-4400
; TELEFAX: (650) 328-4477
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 457 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-834-655-2

Query Match 25.8%; Score 629; DB 2; Length 457;
Best Local Similarity 33.0%; Pred. No. 5.4e-55;
Matches 154; Conservative 76; Mismatches 175; Indels 62; Gaps 13;
Qy 4 REQEHEFFIKDKWCQIDAVLRSHPGGSAITTYKNMDATVTHHTGSKAYOWLT 63
Db 25 KDAEAPFLMIIDNKVYDVREFV-PDHPGGSVILTHVGKDGTDVDFTEH---PEA-AWET 79
Qy 64 ELKKECPQEPPEIPDKDDPKIGDIDVNGNIFNISEKSAQINKSFDTLDMRVRAEGLMD 123

PS Example 2: Pages 105-106; 165pp; English.
CC The present sequence represents a peptide derived from a desaturase
CC enzyme. The specification describes methods for desaturating a
CC fatty acid and for producing a desaturated fatty acid by expressing
CC increased levels of a desaturase. Desaturases can be used for
CC desaturating fatty acids. The enzymes can be used to produce
CC polyunsaturated fatty acids, which can be used for treating malnutrition,
CC in pharmaceutical compositions, in cosmetics or in animal feed. The
CC polyunsaturated fatty acids can be used for treating e.g. restenosis
CC after angioplasty, inflammation, rheumatoid arthritis, asthma, psoriasis,
CC cancer, diabetes or eczema or reduce blood pressure. They can also be
CC used to inhibit platelet aggregation, cause vasodilation, lower
CC cholesterol levels, inhibit proliferation of vessel wall smooth muscle
CC and fibrous tissue, reduce or prevent gastro-intestinal bleeding and
CC other side effects caused by non-steroidal anti-inflammatory drugs,
CC prevent or treat endometriosis and premenstrual syndrome, treat myalgic
CC encephalomyelitis and chronic fatigue after viral infections, treat AIDS,
CC multiple sclerosis, acute respiratory syndrome, hypertension and
CC inflammatory skin disorders.
SQ Sequence 87 AA;

Query Match 11.7%; Score 284.5; DB 1; Length 87;
Best Local Similarity 67.9%; Pred No. 3.8e-22;
Matches 53; Conservative 7; Mismatches 17; Indels 1; Gaps 1;
QY 365 TRNRRPGRTDMLWGLNYQIEHLLFTMPRHNLNTVMPLVKFAAANGLPYMYDDYFTG 424
Db 8 TRNTPSPFIDMLWGLNYQIEHLLFTMPRCNLNRCMKYKWCENNLPLYLVDYFVG 67
QY 425 FWLEIEQFRNIAN-VAAK 441
Db 68 YNLNLOOLKNMAELVQAK 85

Search completed: February 25, 2000, 04:45:46
Job time: 23781 sec

QY 153 LPSAILMGVAMQOLGLWLFHFAHQLFKRNYNDLASVFNFLQFSSGGKQEHNVHH 212
 DB 12 LITAFVLTSAQAGLQHDYCHLSVYRKPKNHLVHFVIGHLKASANWNHRRFOHH 71
 QY 213 AATNVYGRDGLDLPVFFATVAEHLNNYSQDSVWMTLFRMQHVHTFMLPFLRLSLWLOS 272
 DB 72 AKPNIFHKDPDVMNHLVFLGEMQPIEYKGLKLYLPYNHQHEFFLIGPPLIPMYFOY 131
 QY 273 IIFVQMPHYDYRNTAIYEQVGLSLHWASLQGLFLPDWSTRIIMFFLVSHLVGG-- 331
 DB 132 QIIM-----TMIVHKNWVDLAWAYS---YYIRFFITYIPFY---GILGALL 171
 QY 331 -----FLLSH---VVTFNHYSVEKFASSNIMSNYACLOQIMTTRNMRPGRFIDWLWGG 380
 DB 172 FLNIRFLESHWFVWVQTNHIVME---IDQAYRDWFSQLTATCNVEQSFENDWFSGH 228
 QY 381 LNYQIEHHLFTPMRPHNLNTVMPLYKEFAAANGLPY 416
 DB 229 LNFQIEHHLFTPMRPHNLKIAPLVKSLCAKHGIEY 264

RESULT 14

W95513
 ID W95513 standard; Protein: 615 AA.
 AC W95513;
 DE 26-MAR-1999 (first entry)
 KW Amino acid sequence of human desaturase gene contig 2535.
 KW Delta 5 desaturase; recombinant; fatty acid desaturase; FAD; PUFA; oil;
 KW polyunsaturated fatty acid; linoleic acid; arachidonic acid; linolenic;
 KW stearidonic acid; eicosapentaenoic acid; malnutrition; feeding formula;
 KW dietary supplement; prostaglandin; restenosis; angioplasty; inflammation;
 KW rheumatoid arthritis; psoriasis; osteoporosis; cancer; eczema; AIDS;
 KW diabetes; cosmetic; animal feed; human.
 OS Homo sapiens.
 FH Key
 FT Misc_difference 295 Location/Qualifiers
 FT /note= "encoded by TGA"
 FT Misc_difference 321
 FT /note= "encoded by TGA"
 FT Misc_difference 458
 FT /note= "encoded by TGA"
 FT Misc_difference 491
 FT /note= "encoded by TAA"
 FT Misc_difference 517
 FT /note= "encoded by TAG"
 FT Misc_difference 535
 FT /note= "encoded by TGA"
 FT Misc_difference 550
 FT /note= "encoded by TGA"
 FT Misc_difference 615
 FT /note= "encoded by TG"
 PN W09846764-A1.
 PD 22-OCT-1998.
 PF 10-APR-1997; US-956985.
 PR 24-OCT-1997; US-956985.
 PR 11-APR-1997; US-833610.
 PR 11-APR-1997; US-834033.
 PR 11-APR-1997; US-834655.
 PA (ABBO) ABBOTT LAB.
 PA (CALJ) CALGENE LLC.
 PI Chaudhary S, Huang Y, Knutson D, Leonard AE, Mukerji P,
 PI Thurmond J;
 PI WPI: 99-080739/07.
 DR N-PSDB: X00909.
 PT Nucleic acid construct able to express fatty acid desaturase in
 PT plants - useful in human or animal nutrition, as cosmetics and
 PT therapeutically, e.g. for restenosis, cancer and diabetes
 PS Claim 48: Page 167-169; 210pp; English.
 CC The invention relates to a nucleic acid construct that contains at least
 CC one of the nucleotide sequences (X00899 to X00891) encoding Mortierella
 CC alpina delta 6, delta 12 and delta 5 desaturases (W95504 to W95506)
 CC respectively, coupled to an expression control sequence functional in

CC plants. Recombinant plant cells containing at least one DNA encoding a
 CC M. alpina fatty acid desaturase (FAD), can be used for the production of
 CC polyunsaturated fatty acid (PUFA). These recombinant cells or plants
 CC containing them are used to produce oils such as linoleic acid,
 CC arachidonic acid, gamma-linolenic acid, dihomogamma-linolenic acid,
 CC stearidonic acid and eicosapentaenoic acid (EPA). These plant oils are
 CC used: (i) to treat malnutrition; (ii) in infant feeding formulas, or
 CC dietary supplements or substitutes, for use in humans or animals; (iii)
 CC for treating disorders associated with inadequate consumption or
 CC production of PUFA (or their metabolites such as prostaglandins), e.g.
 CC restenosis after angioplasty, inflammation, AIDS, rheumatoid arthritis,
 CC psoriasis, osteoporosis, cancer, eczema, diabetes; (iv) as cosmetics, and
 CC (v) as animal feeds. Fragments of the DNA are used as probes to isolate
 CC related coding sequences. Recombinant plants can produce high yields of
 CC PUFA, since new pathways can be created and unwanted ones suppressed.
 CC Plants can be engineered to express oils of particular PUFA composition,
 CC e.g. one similar to that in human milk, and product recovery is simpler
 CC than with e.g. fish. Sequences W95508-514 represent amino acid sequences
 CC of various contigs of human desaturase genes which are similar to the
 CC M. alpina desaturase sequences.
 SQ Sequence 615 AA;

Query Match 12.8%; Score 312.5; DB 1; Length 615;
 Best Local Similarity 29.0%; Pred. No. 8.9e-24;
 Matches 80; Conservative 46; Mismatches 113; Indels 35; Gaps 6;
 QY 153 LPSAILMGVAMQOLGLWLFHFAHQLFKRNYNDLASVFNFLQFSSGGKQEHNVHH 212
 DB 12 LITAFVLTSAQAGLQHDYCHLSVYRKPKNHLVHFVIGHLKASANWNHRRFOHH 71
 QY 213 AATNVYGRDGLDLPVFFATVAEHLNNYSQDSVWMTLFRMQHVHTFMLPFLRLSLWLOS 272
 DB 72 AKPNIFHKDPDVMNHLVFLGEMQPIEYKGLKLYLPYNHQHEFFLIGPPLIPMYFOY 131
 QY 273 IIFVQMPHYDYRNTAIYEQVGLSLHWASLQGLFLPDWSTRIIMFFLVSHLVGG-- 331
 DB 132 QIIM-----TMIVHKNWVDLAWAYS---YYIRFFITYIPFY---GILGALL 171
 QY 331 -----FLLSH---VVTFNHYSVEKFASSNIMSNYACLOQIMTTRNMRPGRFIDWLWGG 380
 DB 172 FLNIRFLESHWFVWVQTNHIVME---IDQAYRDWFSQLTATCNVEQSFENDWFSGH 228
 QY 381 LNYQIEHHLFTPMRPHNLNTVMPLYKEFAAANGLPY 416
 DB 229 LNFQIEHHLFTPMRPHNLKIAPLVKSLCAKHGIEY 264

RESULT 15

W84144
 ID W84144 standard; Peptide: 87 AA.
 AC W84144;
 DT 15-FEB-1999 (first entry)
 DE Desaturase enzyme peptide sequence.
 KW Fatty acid; desaturase; polyunsaturated fatty acid;
 KW malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis;
 KW cancer; diabetes; eczema; platelet aggregation; vasodilation;
 KW cholesterol level; endometriosis; premenstrual syndrome;
 KW myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;
 KW acute respiratory syndrome; hypertension; inflammatory skin disorder.
 OS Unidentified.
 PN W09846763-A1.
 PD 22-OCT-1998.
 PF 10-APR-1997; US-834655.
 PR 11-APR-1997; US-834655.
 PA (ABBO) ABBOTT LAB.
 PA (CALJ) CALGENE LLC.
 PI Chaudhary S, Huang Y, Knutson D, Leonard AE, Mukerji P,
 PI Thurmond J;
 PI WPI: 98-594582/50.
 DR New isolated fatty acid desaturase enzymes - used for the production
 PT of polyunsaturated fatty acids for use in, e.g. pharmaceutical
 PT compositions, nutritional compositions, cosmetics or animal feed

Db 232 FYEKRLTFDS -LSREFVSQHTFYPIMCAARLNMYVQSILMLTK-----RNVSY 281

QY 292 -IYEQVGLSLHAWNSLQYFLPDNSTRIMFFLVSHLVGFLSHVYTFNHYSVKFAFS 350

Db 282 RAQELGCLVFSFISPLVSLFNGWGERIMFVIASLSVTG-MQOVQFSLNHFSSVY-VG 339

QY 351 SNMSNYACLOQMTTNRMPGRFIDWLWGLNYSQIEHHLFPPTPRNLNTVMPLVKEFAA 410

Db 340 KPGKNNWFKEQDGLDIDSCPPWDMFHGGLQFQIEHHLFPKPRNLRKISPYIELCK 399

QY 411 ANGLPYMVDYFTGFWEIEQFRNTANVAKLTKKI 446

Db 400 KHNLPYNVASFSEKANEMLTLRLNTALQARDITKPL 435

RESULT 12

W84155

ID W84155 standard; Protein: 608 AA.

AC W84155;

DE 15-FEB-1999 (first entry)

DE Human desaturase enzyme encoded by contig 2535.

KW Fatty acid; desaturase; polyunsaturated fatty acid;

KW malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis;

KW cancer; diabetes; eczema; platelet aggregation; vasodilation;

KW cholesterol level; endometriosis; premenstrual syndrome; human;

KW myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;

KW acute respiratory syndrome; hypertension; inflammatory skin disorder.

OS Homo sapiens.

FH Key

FT Location/Qualifiers

FT Misc_difference 608

FT /note= "not specified"

PN W09846763-A1.

PD 22-OCT-1998.

PF 10-APR-1998; U07126.

PR 11-APR-1997; US-834655.

PA (ABBO) ABBOTT LAB.

PA (CALJ) CALGENE LLC.

PI Chaudhary S, Huang Y, Knutzon D, Leonard AE, Mukerji P,

PI Thurmond J;

DR WPI: 98-594582/50.

DR N-PSDB; V63642.

PT New isolated fatty acid desaturase enzymes - used for the production

PT of polyunsaturated fatty acids for use in, e.g. pharmaceutical

PT compositions, nutritional compositions, cosmetics or animal feed

PS Example 12; Pages 123-124; 165pp; English.

CC The present sequence is a human desaturase enzyme. The cDNA sequence was

CC identified based on homology between human cDNA sequences and Mortierella

CC alpina desaturase gene sequences. The specification describes methods for

CC desaturating a fatty acid and for producing a desaturated fatty acid by

CC expressing increased levels of a desaturase. The enzyme can be used for

CC desaturating fatty acids. The enzyme can be used to produce

CC polyunsaturated fatty acids, which can be used for treating malnutrition,

CC in pharmaceutical compositions, in cosmetics or in animal feed. The

CC polyunsaturated fatty acids can be used for treating e.g. restenosis

CC after angioplasty, inflammation, rheumatoid arthritis, asthma,

CC psoriasis, cancer, diabetes or eczema or reduce blood pressure. They

CC can also be used to inhibit platelet aggregation, cause vasodilation,

CC muscle and fibrous tissue, inhibit proliferation of vessel wall smooth

CC and other side effects caused by non-steroidal anti-inflammatory drugs,

CC prevent or treat endometriosis and premenstrual syndrome, treat myalgic

CC encephalomyelitis and chronic fatigue after viral infections, treat

CC AIDS, multiple sclerosis, acute respiratory syndrome, hypertension and

CC inflammatory skin disorders.

CC Sequence 608 AA;

QY 153 LPSAILMGVAMQQLGLWILHEFAHQLFKNRYNDLASVEYGNFLOGFSSGGWKEQHNVHH 212

I : I : : : I I I I : : : : I I I I : I : I : I : I : I

Query Match 12.8%; Score 312.5; DB 1; Length 608;

Best Local Similarity 29.0%; Pred. No. 8.7e-24;

Matches 80; Conservative 46; Mismatches 115; Indels 35; Gaps 6;

Db 12 LITAFVLATSOAQAGLQHDYGHLSVYRKPKNHVLVHKEVIGHLKGASANWNNHRHFQHH 71

QY 213 AATNVVGRDGLDLVFPYATVAEHLNNYSQDSWVMTLFRQHVHMTFMLPFLRLSLQLOS 272

Db 72 AKRNFPHKDPDYNMLHVFVLGEWQPIEYCKKKLKYLPYNNHQHEYFFLIGPLLPIMYFOY 131

QY 273 IIFVSOMPHYDYRYNTAIYEQVGLSLHAWNSLQYFLPDNSTRIMFFLVSHLVGG-- 331

Db 132 QIIM-----TMIVHKNWVDLAWAYS-----YYIRFFITYPEV---GILGALL 171

QY 331 -----FLISH-----VVTFNHYSVEKEFALSSNMSNYACLOQMTTNRMPGRFIDWLG 380

Db 172 FLNFTREFLESHFWVVTQNHIVME---IDQAYRDWFSSQLTATCNVQSFENDWFSGH 228

QY 381 LNYQIEHHLFPTMPRHNLNTVMPLVKEFAAANGLPY 416

Db 229 LNFQIEHHLFPTMPRHNLHKLAPLVKSLCAKHGIEY 264

RESULT 13

W85134

ID W85134 standard; Protein: 608 AA.

AC W85134;

DE 11-FEB-1999 (first entry)

DE A desaturase enzyme encoded by contig 2535.

KW Fatty acid; desaturase; polyunsaturated fatty acid;

KW malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis;

KW cancer; diabetes; eczema; platelet aggregation; vasodilation;

KW cholesterol level; endometriosis; premenstrual syndrome;

KW myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;

KW acute respiratory syndrome; hypertension; inflammatory skin disorder.

OS Homo sapiens.

FH Key

FT Location/Qualifiers

FT Misc_difference 608

FT /note= "not specified"

PN W09846765-A1.

PD 22-OCT-1998.

PF 10-APR-1998; U07422.

PR 11-APR-1997; US-833610.

PA (ABBO) ABBOTT LAB.

PA (CALJ) CALGENE LLC.

PI Chaudhary S, Huang Y, Knutzon D, Leonard AE, Mukerji P,

PI Thurmond J;

DR WPI: 99-009334/01.

DR N-PSDB; V82641.

PT New nucleic acid encoding delta5 and other desaturase enzymes -

PT useful in production of oils of increased arachidonic acid content,

PT used, e.g. for treating cancer, as foods, animal feeds and cosmetics

PS Claim 87; Pages 117-119; 133pp; English.

CC The present sequence represents a human desaturase enzyme. The enzyme

CC sequence is used in the methods of the invention. The specification

CC describes methods for desaturating a fatty acid and for producing a

CC desaturated fatty acid by expressing increased levels of a desaturase.

CC The enzyme can be used for desaturating fatty acids. The enzyme can be

CC used to produce polyunsaturated fatty acids, which can be used for

CC treating malnutrition, in pharmaceutical compositions, in cosmetics or

CC in animal feed. The polyunsaturated fatty acids can be used for treating

CC e.g. restenosis after angioplasty, inflammation, rheumatoid arthritis,

CC asthma, psoriasis, cancer, diabetes or eczema or reduce blood pressure.

CC They can also be used to inhibit platelet aggregation, cause

CC vasodilation, lower cholesterol levels, inhibit proliferation of vessel

CC wall smooth muscle and fibrous tissue, reduce or prevent

CC gastro-intestinal bleeding and other side effects caused by non-steroidal

CC anti-inflammatory drugs, prevent or treat endometriosis and premenstrual

CC syndrome, treat myalgic encephalomyelitis and chronic fatigue after

CC viral infections, treat AIDS, multiple sclerosis, acute respiratory

CC syndrome, hypertension and inflammatory skin disorders.

CC Sequence 608 AA;

QY 312 QIIM-----TMIVHKNWVDLAWAYS-----YYIRFFITYPEV---GILGALL 171

I : I : : : I I I I : : : : I I I I : I : I : I : I : I

Query Match 12.8%; Score 312.5; DB 1; Length 608;

Best Local Similarity 29.0%; Pred. No. 8.7e-24;

Matches 80; Conservative 46; Mismatches 115; Indels 35; Gaps 6;

OS Borago officinalis.
FH Key Location/Qualifiers
FT Binding_site 40..44
FT Binding_site /note="cytochrome b5 haem-binding motif"
FT Binding_site 156..163
FT Binding_site /note="metal binding, histidine-rich motif"
FT Binding_site 196..200
FT Binding_site /note="metal binding, histidine-rich motif"
FT Binding_site 373..377
FT Binding_site /note="metal binding, histidine-rich motif"
PD WO9845461-A1.
PN 15-OCT-1998.
PF 09-APR-1998; U07179.
PR 09-APR-1997; US-831575.
PA (RHON) RHONE-POULENC AGROCHIMIE.
PI Li Z, Thomas TL;
DR WPI; 99-180333/15.
DR N-PSDB; X24917.
DR Nucleic acid containing oleosin 5'-regulatory region - useful for
PT modulating fatty acid synthesis and lipid metabolism in plants,
PT particularly to increase content of gamma-linolenic acid
PS Example 2; Page 61; 101pp; English.
CC The present sequence is borage delta-6 desaturase, an enzyme that
CC catalyzes the conversion of linoleic acid to gamma-linolenic acid
CC (GLA). Delta-6 desaturase cDNA (see X24917) was isolated from a
CC borage membrane-bound polysomal cDNA library using a partial clone,
CC obtained from an EST database search, as probe. The borage delta-6
CC desaturase nucleic acid can be operably linked to the seed-specific
CC 5' regulatory region (see X24916) of the Arabidopsis thaliana
CC oleosin At521 gene in claimed expression cassettes of the invention.
CC Transgenic plants, e.g. sunflower, soybean, maize, tobacco, cotton,
CC peanut, oilseed rape or Arabidopsis are obtained that show increased
CC levels of GLA or octadecatrienoic acid. The levels of desirable
CC fatty acids in oilseed crops can be manipulated to provide seed
CC oils of use in human health and industrial applications.
SQ Sequence 448 AA;

Query Match 16.8%; Score 409.5; DB 1; Length 448;
Best Local Similarity 27.2%; Pred. No. 5.4e-34;
Matches 124; Conservative 69; Mismatches 198; Indels 65; Gaps 16;

QY 12 FIKIDGKCQIDDAVLRSHPGGS-AITYKNMDATTVFHTGTSKEAYOMLTELKKECP 70
DB 24 WISIQKAYDVSQWV-KDHPGGSPLKSLAGQEVDTAFVAFHPAS-----TW----- 70
QY 71 TQPEIPDKDDPIKIDDDVNMGTNISEKRSQAQINKSFTDLRMVRRAEGLMDG----- 125
DB 70 -----KNLDKFTTG-YLKDYSVSEVSKDYRKLVFEFSKMGLYDKKGHIMF 114
QY 125 SPLFYIRKILE-TIFTILFAFYLOHYTYLPSAILMGVAQOGLWLIHEFAHOLFKNRY 183
DB 115 ATLCFIAMLFAMSYGVLFCEGLVHLF---SGCLMGLFWIQSGWIGHDAGHYVMVSDSR 171
QY 184 YNDLASVFGNFIQGGSGGKQHNHHAATNVVGRGDLDLP-----FYATVAEH 236
DB 172 LNKFMGIFAANCLSGISIGMKNHNAHIAACNSLEYDPDLQYIPFLVSVSSKFFGSLTSH 231
QY 237 L--NNYSQDSQWMTLFRQHVHTF--MLPFLRLSWLLOSIFVQSMPTHYDYRNTA- 292
DB 232 FYEKRLTFDS--LSRFFVSQYHWTFTYIMCAARLNMVQSLMLTK-----RNVSYS 281
QY 292 -IYEOVGLSLHWASLQGLYLPDWSRIMFPLVSHLVGGFLSHVTFNHSYVEKFAIS 350
DB 282 RAQELLGLCFVSIPIYPLLVSCPLNNGERIMFVIASLSVTG-MQVQFSLNHFSSVY-VG 339
QY 351 SNIMSNACLIQIMTRNNRGRFIDWLMGGLNYQIEHLFTPTMPRHNTNMYPLVKEFAA 410
DB 340 KPGNNFEEKOTDGLDLSICPPWMDWTFHGGLOFQIEHLFPKMPRCNLKISPPYIELCK 399
QY 411 ANGLPVMDDYFTGFWEIEQFRNTANVAALKTKI 446
DB 400 KHNLPYNVASFKANEMTLRLRLNTALQARDITKPL 435

RESULT 11
W85122
ID W85122 standard; Protein: 446 AA.
AC W85122;
DT 11-FEB-1999 (first entry)
DE A delta-6 desaturase enzyme amino acid sequence.
KW Fatty acid; delta-6 desaturase; polyunsaturated fatty acid;
KW malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis;
KW cancer; diabetes; eczema; platelet aggregation; vasodilation;
KW cholesterol level; endometriosis; premenstrual syndrome;
KW myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;
KW acute respiratory syndrome; hypertension; inflammatory skin disorder.
OS Unidentified.
PN WO9846765-A1.
PD 22-OCT-1998.
PF 10-APR-1998; U07422.
PR 11-APR-1997; US-833610.
PA (ABBO) ABBOTT LAB.
PI (CALJ) CALGENE LLC.
PI Chaudhary S, Huang Y, Knutson D, Leonard AE, Mukerji P,
PI Thurmond J;
DR WPI; 99-009334/01.
PT New nucleic acid encoding delta5 and other desaturase enzymes -
PT useful in production of oils of increased arachidonic acid content,
PT used, e.g. for treating cancer, as foods, animal feeds and cosmetics
PT disclosure; Pages 96-98; 153pp; English.
PS The present sequence represents a fatty acid delta-6 desaturase enzyme.
CC The specification describes methods for desaturating a fatty acid and
CC for producing a desaturated fatty acid by expressing increased levels of
CC a desaturase. The present desaturase is an enzyme which introduces a
CC double bond carbons 6 and 7 from the carboxyl end of a fatty acid
CC molecule. The enzyme can be used for desaturating fatty acids. The
CC enzyme can be used to produce polyunsaturated fatty acids, which can
CC be used for treating malnutrition, in pharmaceutical compositions,
CC in cosmetics or in animal feed. The polyunsaturated fatty acids can
CC be used for treating e.g. retinosis after angioplasty, inflammation,
CC rheumatoid arthritis, asthma, psoriasis, cancer, diabetes or eczema
CC or reduce blood pressure. They can also be used to inhibit platelet
CC aggregation, cause vasodilation, lower cholesterol levels, inhibit
CC proliferation of vessel wall smooth muscle and fibrous tissue,
CC reduce or prevent gastro-intestinal bleeding and other side effects
CC caused by non-steroidal anti-inflammatory drugs, prevent or treat
CC endometriosis and premenstrual syndrome, treat myalgic encephalomyelitis
CC and chronic fatigue after viral infections, treat AIDS, multiple
CC sclerosis, acute respiratory syndrome, hypertension and inflammatory skin
CC disorders.
SQ Sequence 446 AA;

Query Match 16.7%; Score 407.5; DB 1; Length 446;
Best Local Similarity 27.2%; Pred. No. 8.6e-34;
Matches 124; Conservative 69; Mismatches 198; Indels 65; Gaps 16;

QY 12 FIKIDGKCQIDDAVLRSHPGGS-AITYKNMDATTVFHTGTSKEAYOMLTELKKECP 70
DB 24 WISIQKAYDVSQWV-KDHPGGSPLKSLAGQEVDTAFVAFHPAS-----TW----- 70
QY 71 TQPEIPDKDDPIKIDDDVNMGTNISEKRSQAQINKSFTDLRMVRRAEGLMDG----- 125
DB 70 -----KNLDKFTTG-YLKDYSVSEVSKDYRKLVFEFSKMGLYDKKGHIMF 114
QY 125 SPLFYIRKILE-TIFTILFAFYLOHYTYLPSAILMGVAQOGLWLIHEFAHOLFKNRY 183
DB 115 ATLCFIAMLFAMSYGVLFCEGLVHLF---SGCLMGLFWIQSGWIGHDAGHYVMVSDSR 171
QY 184 YNDLASVFGNFIQGGSGGKQHNHHAATNVVGRGDLDLP-----FYATVAEH 236
DB 172 LNKFMGIFAANCLSGISIGMKNHNAHIAACNSLEYDPDLQYIPFLVSVSSKFFGSLTSH 231
QY 237 L--NNYSQDSQWMTLFRQHVHTF--MLPFLRLSWLLOSIFVQSMPTHYDYRNTA- 292

/label= Metal_box-2					
FN	WO9621022-A2.				
PD	11-JUL-1996.				
PF	28-DEC-1995; IB1167.				
PR	30-DEC-1994; US-366779.				
PA	(RHON) RHONE POULENC AGROCHIMIE.				
PI	Freyssinet GL, Nuccio M, Nunberg AN, Reddy AS, Thomas TL;				
DR	WPI; 96-333997/33.				
DR	N-PSDB; T30395.				
PT	Transgenic plants comprising the borage delta-6-desaturase gene				
PT	show increased production of gamma linolenic acid and having				
PT	increased resistance to chilling				
PS	Claim 3; Page 52-53; 75pp; English.				
CC	Borage delta-6-desaturase (R98455) catalyses the conversion of				
CC	linoleic acid to gamma-linolenic acid (GLA). Its sequence was				
CC	deduced from that of the delta-6-desaturase gene (T30395) isolated				
CC	from a borage membrane-bound polysomal library. The sequence is				
CC	distinct from that of Synecchocystis delta-6-desaturase (R98456).				
CC	Expression of the desaturase in transgenic plants, esp. sunflower,				
CC	soybean, maize, tobacco, peanut, carrot or oilseed rape, results in				
CC	increased GLA prodn. Alteration of the plant membrane lipids as a				
CC	result of expression of the desaturase may also result in increased				
CC	resistance to chilling.				
SQ	Sequence 448 AA;				
Query Match		16.8%;	Score 409.5;	DB 1;	Length 448;
Best Local Similarity		27.2%;	Pred. No. 5.4e-34;		
Matches 124;		Conservative 69;	Mismatches 198;	Indels 65;	Gaps 16;
QY	12 FTKIDGKCQICDADVLRSHPGGS-AITTYKNMDATVFTHTFGSKAYOWLTCLKKECP	70			
Db	24 WSIQCKAYDVSDMW-KDHPPGSEFLKSLAGOEVDADFAPHAS-----TW-----	70			
QY	71 TQEPEIDKDPKIGIDDVNGMTNISKRSAQINKSFDTLRMRVRAEGLMDG-----	125			
Db	70 -----KNLKDFFTG-YLLKDYSYSEVS KDYRLVFEEFSKMGLYDKKGHLMF	114			
QY	125 SPLFYRKILE-TITILFAFLQVHTYYLPASAILMGVAWQOLGLWIIHEFAHHOLFKNRY	183			
Db	115 ATLFCIAMLFAMSVYGVLFCGVLVHLF---SGCLMGLFWIQSGWIGHDAGHYMVVSDSR	171			
QY	184 YNDLASYPVGNFLOGFSSGGWKEOHNVHHAATNYYGRDGLDLVP-----FYATAEH	236			
Db	172 LNKFMGFIAANCLSGISIGMKWNHNAAHIACNSLEYPDLOIYLPFLVVSKFFGSTJSH	231			
QY	237 L--NNYSODSMVTMLFRKHQVHWTF--MLPFLRSLULLQSIFIVSQMPHTYIDYRNTA-	292			
Db	232 FYEKRLTDS--LSRFVFSVOHQHTFYIPMCARLNMYVQSLMLLTK-----RVNSY	281			
QY	292 -IYEQVGLSLHWAWSLGQLYFLPDWSTRIMFELVSHLVGGFLLSHVYTFNHYSVEKFALS	350			
Db	282 RAQELLGCLVFSIWYPLLVSCLPNWGERIMFVASLTSVTG-MQQOVQFSLNHFSSSVY-VG	339			
QY	351 SNTMSNVACLOIMTRNMRCGRFITDWLWGGLNQIEHLEFPTMPRHNLNVMPLVKFEAA	410			
Db	340 KPGKGNWFEXQTDCGLDISCPPWMDFHGGLQGQIEHLEFPKPRCNLRKISPYIELCK	399			
QY	411 ANGCLPYMDDYFGFWGLEIQCFRNIANVAKLTKKI 446				
Db	400 KHNLPNYASFSPANEMTURLTLNTALQARDITKPL 435				
RESULT	9				
W67471	ID	W67471 standard; Protein; 448 AA.			
AC	W67471;				
DT	02-MAR-1999 (first entry)				
DE	Borage delta-6 desaturase protein.				
KW	Upstream region; regulatory region; sunflower; albumin; seed; expression;				
OS	lipid metabolism; delta-6 desaturase; transgenic plant.				
EFH	Borago officinalis.				
Key	Location/Qualifiers				

CC containing them are used to produce oils such as linoleic acid, ...
CC arachidonic acid, gamma-linolenic acid, dihomogamma-linolenic acid,
CC stearidonic acid and eicosapentaenoic acid (EPA). These plant oils are
CC used: (i) to treat malnutrition; (ii) in infant feeding formulas, or
CC dietary supplements or substitutes, for use in humans or animals; (iii)
CC for treating disorders associated with inadequate consumption or
CC production of PUFA (or their metabolites such as prostaglandins), e.g.
CC restenosis after angioplasty, inflammation, AIDS, rheumatoid arthritis,
CC psoriasis, osteoporosis, cancer, eczema, diabetes; (iv) as cosmetics, and
CC (v) as animal feeds. Fragments of the DNA are used as probes to isolate
CC related coding sequences. Recombinant plants can produce high yields of
CC PUFA, since new pathways can be created and unwanted ones suppressed.
CC Plants can be engineered to express oils of particular PUFA composition,
CC e.g. one similar to that in human milk, and product recovery is simpler
CC than with e.g. fish. Sequences W95508-514 represent amino acid sequences
CC of various contigs of human desaturase genes which are similar to the
CC M. alpina desaturase sequences.
SQ Sequence 753 AA;

Query Match 16.9%; Score 412; DB 1; Length 753;
Best Local Similarity 27.0%; Pred. No. 6.4e-34;
Matches 116; Conservative 65; Mismatches 170; Indels 78; Gaps 11;

QY 18 KWCQIDDAV-----LRSHPGGS-AITTYKNMDATTVFHTFHTGSKRAYOWLT-----EL 65
DB 22 RLVVIDKVVNISEFTRHRRGGSRVISHYAGODATDFVAFHINKGLVKYMNILLIGEL 81
QY 66 KKECTOEPIDKDDPIKIGIDVNMGTNISEKSAQINKSTDLRMVRRAEGLMDGS 125
DB 82 SPEQSPFEP-----TKNKELTDEFELRATVERMGLKAN 116
QY 126 PLFYRKILETI-----FTLFAFYLOYHTYILPSAILMGVANOQLGWLHIEFAHOLF 179
DB 117 HVFFLLYLLHLLDGAALTLVWFGTSFLPFLCAVLLSAVOQAQAGWLQHDYGHLSVY 176
QY 180 KRYNDLASVYGVNQLGSSGGKQBNVHHAATNVVGRDGLDLVPFATVAEHLNN 239
DB 177 RKPKNHLLVHKFVIGHLKGASANNHRRHFOHAKPNIFHKDPDVMNMLHVFVLGEWQPIE 236
QY 240 YSDQSVWMTLFRWQHVTMFLPFLRLSLWLSQIFVSQMPHTYDYIRNTATYEQVGLS 299
DB 237 YGKKKLYLPYNHQHEVFFLIGPLLPMPYQYQIIM-----TMIHKNWVD 283
QY 300 LHWANSLGOLYFLPDWSTRMFFLVSHLVGG-----FLLSH-----VVFNFHYSVEKF 347
DB 284 LAWAVS-----YYIRFFITYIPFY---GILGALLFLNFRFLESHWFWVWVTONNHVME-- 335
QY 348 ALSSNMSNYACLOIMTTRNMRPGRFDLWGLGNLYQTEHHLFTMPRHNLTVMPLVKE 407
DB 335 -IDQAYRDWFSSQLTATCNVEQSFNDWFGSHLNFQIEHHLFTMPRHNLTVMPLVKS 393
QY 408 FAANGLPY 416
DB 394 LCAKHGIEY 402

RESULT 8
R98455
ID R98455 standard; Protein; 448 AA.
AC R98455;
DT 15-SEP-1996 (first entry)
DE Borage delta-6-desaturase.
KW Delta-6-desaturase; gamma-linolenic acid; transgenic plant; borage;
KW polyunsaturated fatty acid; octadecatetraenoic acid;
KW chilling resistance; oilseed.
OS Borage officinalis.
FH Key Location/Qualifiers
FT 156..163
FT /label= Lipid_box
FT 196..200
FT /label= Metal_box-1
FT 372..377

DB 177 RKPKNHLLVHKFVIGHLKGASANNHRRHFOHAKPNIFHKDPDVMNMLHVFVLGEWQPIE 236
QY 240 YSDQSVWMTLFRWQHVTMFLPFLRLSLWLSQIFVSQMPHTYDYIRNTATYEQVGLS 299
DB 237 YGKKKLYLPYNHQHEVFFLIGPLLPMPYQYQIIM-----TMIHKNWVD 283
QY 300 LHWANSLGOLYFLPDWSTRMFFLVSHLVGG-----FLLSH-----VVFNFHYSVEKF 347
DB 284 LAWAVS-----YYIRFFITYIPFY---GILGALLFLNFRFLESHWFWVWVTONNHVME-- 335
QY 348 ALSSNMSNYACLOIMTTRNMRPGRFDLWGLGNLYQTEHHLFTMPRHNLTVMPLVKE 407
DB 335 -IDQAYRDWFSSQLTATCNVEQSFNDWFGSHLNFQIEHHLFTMPRHNLTVMPLVKS 393
QY 408 FAANGLPY 416
DB 394 LCAKHGIEY 402

RESULT 7
W95514
ID W95514 standard; Protein; 753 AA.
AC W95514;
DT 26-MAR-1999 (first entry)
DE Amino acid sequence of human desaturase gene contig 253538a.
KW Delta 5 desaturase; recombinant; fatty acid desaturase; FAD; PUFA; oil;
KW polyunsaturated fatty acid; linoleic acid; arachidonic acid; linolenic;
KW stearidonic acid; eicosapentaenoic acid; malnutrition; feeding formula;
KW dietary supplement; prostaglandin; restenosis; angioplasty; inflammation;
KW rheumatoid arthritis; psoriasis; osteoporosis; cancer; eczema; AIDS;
KW diabetes; cosmetic; animal feed; human.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Misc_difference 433 /note= "encoded by TGA"
FT Misc_difference 459 /note= "encoded by TGA"
FT Misc_difference 596 /note= "encoded by TGA"
FT Misc_difference 629 /note= "encoded by TGA"
FT Misc_difference 655 /note= "encoded by TAA"
FT Misc_difference 673 /note= "encoded by TAG"
FT Misc_difference 688 /note= "encoded by TGA"
FT Misc_difference 753 /note= "encoded by TGA"
FT Misc_difference 753 /note= "encoded by TG"
PN W9846764-A1.
PD 22-OCT-1998.
PF 10-APR-1998; U07421.
PR 24-OCT-1997; US-956985.
PR 11-APR-1997; US-833610.
PR 11-APR-1997; US-834033.
PR 11-APR-1997; US-834655.
PA (ABBO) ABBOTT LAB.
PA (CALJ) CALGENE LLC.
PI Chaudhary S, Huang Y, Knutzon D, Leonard AE, Mukerji P,
PI Thurmond J;
DR N-PSDB: X00910.
DR WPI: 99-080739/07.
PT Nucleic acid construct able to express fatty acid desaturase in
PT plants - useful in human or animal nutrition, as cosmetics and
PT therapeutically, e.g. for restenosis, cancer and diabetes
PS Claim 48; page 169-171; 210pp; English.
CC The invention relates to a nucleic acid construct that contains at least
CC one of the nucleotide sequences (X00889 to X00891) encoding Mortierella
CC alpina delta 6, delta 12 and delta 5 desaturases (W95504 to W95506)
CC respectively, coupled to an expression control sequence functional in
CC plants. Recombinant plant cells containing at least one DNA encoding a
CC M. alpina fatty acid desaturase (FAD), can be used for the production of
CC polyunsaturated fatty acid (PUFA). These recombinant cells or plants

OS Homo sapiens. Location/Qualifiers
 FT Misc_difference 746 /note= "not specified"
 PN WO9846763-A1.
 PD 22-OCT-1998.
 PF 10-APR-1998; U07126.
 PR 11-APR-1997; US-834655.
 PA (ABBO) ABBOTT LAB.
 PI (CALJ) CALGENE LLC.
 PI Chaudhary S, Huang Y, Knutzon D, Leonard AE, Mukerji P,
 PI Thurmmond J;
 DR WPI: 98-594582/50.
 DR N-PSDB: V63643.
 PR New isolated fatty acid desaturase enzymes - used for the production
 PT of polyunsaturated fatty acids for use in, e.g. pharmaceutical
 PT compositions, nutritional compositions, cosmetics or animal feed
 PS Example 12: Pages 124-126; 155pp; English.
 CC The present sequence is a human desaturase enzyme. The cDNA sequence was
 CC identified based on homology between human cDNA sequences and Mortierella
 CC alpina desaturase gene sequences. The specification describes methods for
 CC desaturating a fatty acid and for producing a desaturated fatty acid by
 CC expressing increased levels of a desaturase. The enzyme can be used for
 CC desaturating fatty acids. The enzyme can be used to produce
 CC polyunsaturated fatty acids, which can be used for treating malnutrition,
 CC in pharmaceutical compositions, in cosmetics or in animal feed. The
 CC polyunsaturated fatty acids can be used for treating e.g. restenosis
 CC after angioplasty, inflammation, rheumatoid arthritis, asthma,
 CC psoriasis, cancer, diabetes or eczema or reduce blood pressure. They
 CC can also be used to inhibit platelet aggregation, cause vasodilation,
 CC lower cholesterol levels, inhibit proliferation of vessel wall smooth
 CC muscle and fibrous tissue, reduce or prevent gastro-intestinal bleeding
 CC and other side effects caused by non-steroidal anti-inflammatory drugs,
 CC prevent or treat endometriosis and premenstrual syndrome, treat myalgic
 CC encephalomyelitis and chronic fatigue after viral infections, treat
 CC AIDS, multiple sclerosis, acute respiratory syndrome, hypertension and
 CC inflammatory skin disorders.
 CC Sequence 746 AA;

Query Match 16.9%; Score 412; DB 1; Length 746;
 Best Local Similarity 27.0%; Pred. No. 6.3e-34;
 Matches 116; Conservative 65; Mismatches 170; Indels 78; Gaps 11;

QY 18 KWCQIDDAV-----LRSHPGGS-AITTKNDATTFTHTGSKAEYQWLT-----EL 65
 DB 22 RNLVIDRKVYNISEFTRRHPPGGSRVISHYAGODATDPFVAFHINKGLVKYKNSLLIGEL 81
 QY 66 KKECPTQPEIPDKDDPIKIGIDVNMGTNFNISEKRSQAINKSFDTLDMRVRAEGLMDGS 125
 DB 82 SPOQPSFEP-----TKNKELTDEFRELATRVEMGLMKAN 116
 QY 126 PLFYIRKILETI-----FTILFAFYLYQHTYTLPSAILMGVAMQQLGWLIHEFAHOLF 179
 DB 117 HVFFLLVLLHLLDGAAMLTLWVGTSLFPLLCVALLSAVQQAQAGWLQHDYGHLSVY 176
 QY 180 KNYRYNDLASVFNQFLOGSSGKWEQHNHHAATNVGRDGLDLPVFPYATVAEHLNN 239
 DB 177 RPKWNHLVHKFVICHKLKASANNHRRHQHAKPNIFHKDPDYNMLRVFVILGEWQIE 236
 QY 240 YSDSWYMTLFRWQHVTMFLPFLRLSWLLOSIFFVSQMTHTYDYIRNTAIVEQVGLS 299
 DB 237 YGKKKLYLPNHQHEFFLLGPPLLIPMYFYQIIM-----TMIVHKNWVD 283
 QY 300 LHWAMSGQLYFLPDWSTIRMFVLSHLVG-----FLLSH-----VTFNHYSEKFP 347
 DB 284 LAWAVS-----YYIRFFITYPFY---GILGALLEFNIRFLESFWVMTOMNHVME-- 335
 QY 348 ALSNMSNVACIQMTRNMRGRFIDWLWGLNLYQIEHFLFTMPRHNLTNVPVLKE 407
 DB 335 -IDQAYRDWFSSQLTATCNVEQSFNDWFSGLHNFQIEHFLFTMPRHNLTNVPVLKE 407
 QY 408 FAANGLPY 416

Db 394 LCAKHGIEY 402

RESULT 6

W85135 ID W85135 standard; Protein; 746 AA.
 AC W85135;
 DT 11-FEB-1999 (first entry)
 DE A desaturase enzyme encoded by contig 253538a.
 KW Fatty acid; desaturase; polyunsaturated fatty acid;
 KW malnutrition; inflammation; rheumatoid arthritis;
 KW cancer; diabetes; eczema; platelet aggregation; vasodilation;
 KW cholesterol level; endometriosis; premenstrual syndrome;
 KW myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;
 KW acute respiratory syndrome; hypertension; inflammatory skin disorder.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Misc_difference 746 /note= "not specified"
 PN WO9846765-A1.
 PD 22-OCT-1998.
 PF 10-APR-1998; U07422.
 PR 11-APR-1997; US-833610.
 PA (ABBO) ABBOTT LAB.
 PI (CALJ) CALGENE LLC.
 PI Chaudhary S, Huang Y, Knutzon D, Leonard AE, Mukerji P,
 PI Thurmmond J;
 DR WPI: 99-009334/01.
 DR N-PSDB: V83642.
 PR New nucleic acid encoding delta5 and other desaturase enzymes -
 PT useful in production of oils of increased arachidonic acid content,
 PT used, e.g. for treating cancer, as foods, animal feeds and cosmetics
 PS Claim 87; Pages 119-120; 153pp; English.
 CC The present sequence represents a human desaturase enzyme. The enzyme
 CC sequence is used in the methods of the invention. The specification
 CC describes methods for desaturating a fatty acid and for producing a
 CC desaturated fatty acid by expressing increased levels of a desaturase.
 CC The enzyme can be used for desaturating fatty acids, which can be used for
 CC treating malnutrition, in pharmaceutical compositions, in cosmetics or
 CC in animal feed. The polyunsaturated fatty acids can be used for treating
 CC e.g. restenosis after angioplasty, inflammation, rheumatoid arthritis,
 CC asthma, psoriasis, cancer, diabetes or eczema or reduce blood pressure.
 CC They can also be used to inhibit platelet aggregation, cause
 CC vasodilation, lower cholesterol levels, inhibit proliferation of vessel
 CC wall smooth muscle and fibrous tissue, reduce or prevent
 CC gastro-intestinal bleeding and other side effects caused by non-steroidal
 CC anti-inflammatory drugs, prevent or treat endometriosis and premenstrual
 CC syndrome, treat myalgic encephalomyelitis and chronic fatigue after
 CC viral infections, treat AIDS, multiple sclerosis, acute respiratory
 CC syndrome, hypertension and inflammatory skin disorders.
 CC Sequence 746 AA;

Query Match 16.9%; Score 412; DB 1; Length 746;
 Best Local Similarity 27.0%; Pred. No. 6.3e-34;
 Matches 116; Conservative 65; Mismatches 170; Indels 78; Gaps 11;

QY 18 KWCQIDDAV-----LRSHPGGS-AITTKNDATTFTHTGSKAEYQWLT-----EL 65
 DB 22 RNLVIDRKVYNISEFTRRHPPGGSRVISHYAGODATDPFVAFHINKGLVKYKNSLLIGEL 81
 QY 66 KKECPTQPEIPDKDDPIKIGIDVNMGTNFNISEKRSQAINKSFDTLDMRVRAEGLMDGS 125
 DB 82 SPOQPSFEP-----TKNKELTDEFRELATRVEMGLMKAN 116
 QY 126 PLFYIRKILETI-----FTILFAFYLYQHTYTLPSAILMGVAMQQLGWLIHEFAHOLF 179
 DB 117 HVFFLLVLLHLLDGAAMLTLWVGTSLFPLLCVALLSAVQQAQAGWLQHDYGHLSVY 176
 QY 180 KNYRYNDLASVFNQFLOGSSGKWEQHNHHAATNVGRDGLDLPVFPYATVAEHLNN 239

CC for producing a desaturated fatty acid by expressing increased levels of
 CC a desaturase. The present desaturase is an enzyme which introduces a
 CC double bond carbons 6 and 7 from the carboxyl end of a fatty acid
 CC molecule. The enzyme can be used for desaturating fatty acids. The
 CC enzyme can be used to produce polyunsaturated fatty acids, which can
 CC be used for treating malnutrition, in pharmaceutical compositions,
 CC in cosmetics or in animal feed. The polyunsaturated fatty acids can
 CC be used for treating e.g. restenosis after angioplasty, inflammation,
 CC rheumatoid arthritis, asthma, psoriasis, cancer, diabetes or eczema
 CC or reduce blood pressure. They can also be used to inhibit platelet
 CC aggregation, cause vasodilation, lower cholesterol levels, inhibit
 CC proliferation of vessel wall smooth muscle and fibrous tissue,
 CC reduce or prevent gastro-intestinal bleeding and other side effects
 CC caused by non-steroidal anti-inflammatory drugs, prevent or treat
 CC endometriosis and premenstrual syndrome, treat myalgic encephalomyelitis
 CC and chronic fatigue after viral infections, treat AIDS, multiple
 CC sclerosis, acute respiratory syndrome, hypertension and inflammatory skin
 CC disorders.
 CC Sequence 457 AA:

Query Match 25.5%; Score 620; DB 1; Length 457;
 Best Local Similarity 32.8%; Pred. No. 1e-55;
 Matches 153; Conservative 76; Mismatches 176; Indels 62; Gaps 13;

QY 4 REQHEPFFIKIDKWCQIDDAVLRSHPGGSAITTYKNNDAITVFHTFTGSKAYQWLT 63
 DB 25 KKDAEAPFLMIDNKVDYREFV-PDHGGSVILTHVGKDGTDVETPH---PER-AWET 79
 QY 64 ELKKECPQPEIPDKDPIKIDGVNNGTFTNISEKSAQINKSFDDLRMRVRAEGLMD 123
 DB 80 LANFVVGDI DESDRDIKNDDE-----AAEVRK-----LRTLFQSLGYD 118
 QY 124 GSPFLYIRKI-----LETIFTLFAFYLOYHTY-YLPSAILMGVAQOGLWLIHEFAHQ 177
 DB 119 SSKAYAFKVSFNLGSLGSLTVIVAKWGOTSTLANVLSAALGLFVQCGWLAHDFLHQ 178
 QY 178 LFNRYNDLASYFYVGNFLQFSSGGKQHNHVAATNVGRDGLDLPFYATVAEHL 237
 DB 179 VFQDFWGLDLCFALGGVCGFSSSWKDKHNTHAAPNVHVEDPDIDTHPL-LTWSEHA 237
 QY 238 NNYSD-----SWMTLFRQHVHTF--MLPFLRLSWLLSIIIV-----SQ 278
 DB 238 LEMFSDVPDEELTRMWSRMLNQTWTFYFPLSLFARLSWCLQSILFVLPNGQAKPSGAR 297
 QY 279 MPTHYDYRYNTAIYEOVGLSLHWAWSLGLY-FLPDWSTRIIMFVLVSHVGGLSHVY 337
 DB 298 VP-----ISLVEQLSLAMHHTWYLATMFLFKDPVNMVLYFLVSOAVCGNLLAIYF 348
 QY 338 TFNHSYVEKFSALSSNMSYACLIQIMTRMRPGRFIDMLWGGLNYQIEHHLFPTMPRH 397
 DB 349 SLNHGMPVISKEEAVDMDFTKQIITGRDVPGLFANFTGGLNYQIEHHLFPTMPRH 408
 QY 398 LNTVMPLVKEFAAANGPLVMYDDYFTGFWLEIEQFRNIANYAAKLTK 444
 DB 409 FSKIQPAVETLCKKYNVRYHTTGMEGTAEVFSRLNEVSKAASKMGK 455

RESULT 4
 W84139
 ID W84139 standard; Peptide: 355 AA.
 AC W84139;
 DT 15-FEB-1999 (first entry)
 DE Desaturase enzyme peptide sequence.
 KW Fatty acid; desaturase; polyunsaturated fatty acid;
 KW malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis;
 KW cancer; diabetes; eczema; platelet aggregation; vasodilation;
 KW cholesterol level; endometriosis; premenstrual syndrome;
 KW myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;
 KW acute respiratory syndrome; hypertension; inflammatory skin disorder.
 OS Unidentified.
 PN W09846763-A1.
 PD 22-OCT-1998.

FF 10-APR-1998; U07126.
 FR 11-APR-1997; US-834655.
 PA (ARBO) ABBOTT LAB.
 PA (CALJ) CALGENE LLC.
 PI Chaudhary S, Huang Y, Knutzon D, Leonard AE, Mukerji P,
 PI Thurmond J;
 DR WPI; 98-594592/50.

DR New isolated fatty acid desaturase enzymes - used for the production
 of polyunsaturated fatty acids for use in, e.g. pharmaceutical
 compositions, nutritional compositions, cosmetics or animal feed
 PT Example 2: Pages 101-102; 165pp; English.
 PS The present sequence represents a peptide derived from a desaturase
 CC enzyme. The specification describes methods for desaturating a
 CC fatty acid and for producing a desaturated fatty acid by expressing
 CC increased levels of a desaturase. Desaturases can be used for
 CC desaturating fatty acids. The enzymes can be used to produce
 CC polyunsaturated fatty acids, which can be used for treating malnutrition,
 CC in pharmaceutical compositions, in cosmetics or in animal feed. The
 CC polyunsaturated fatty acids can be used for treating e.g. restenosis
 CC after angioplasty, inflammation, rheumatoid arthritis, asthma, psoriasis,
 CC cancer, diabetes or eczema or reduce blood pressure. They can also be
 CC used to inhibit platelet aggregation, cause vasodilation, lower
 CC cholesterol levels, inhibit proliferation of vessel wall smooth muscle
 CC and fibrous tissue, reduce or prevent gastro-intestinal bleeding and
 CC other side effects caused by non-steroidal anti-inflammatory drugs,
 CC prevent or treat endometriosis and premenstrual syndrome, treat myalgic
 CC encephalomyelitis and chronic fatigue after viral infections, treat AIDS,
 CC multiple sclerosis, acute respiratory syndrome, hypertension and
 CC inflammatory skin disorders.
 CC Sequence 355 AA;

Query Match 22.8%; Score 555; DB 1; Length 355;
 Best Local Similarity 34.5%; Pred. No. 3.6e-49;
 Matches 124; Conservative 65; Mismatches 134; Indels 36; Gaps 8;

QY 112 LMRVRAEGLMDGSLFYIRKI-----LETIFTLFAFYLOYHTY-YLPSAILMGVAQO 165
 DB 5 LRTLFQSLGYDSSKAYAFKVSFNLGSLGSLTVIVAKWGOTSTLANVLSAALGLFVQO 64
 QY 166 LGWLHTEFAHOLFKNRYNDLASYFVGNFLQFSSGGKQHNHVAATNVYGRDGLD 225
 DB 65 CGWLHADFLLHQVDFQDFWGLDLCFALGGVCGFSSSWKDKHNTHAAPNVHGEDPDID 124
 QY 226 LVPFYATVAEHLNNSQD-----SWMTLFRQHVHTF--MLPFLRLSWLLSIIIV- 277
 DB 125 THPL-LTWSEHALEMFSDVPDEELTRMWSRMLNQTWTFYFPLSLFARLSWCLQSILFVL 183
 QY 277 -----SQMPTHYDYRYNTAIYEOVGLSLHWAWSLGLY-FLPDWSTRIIMFVLV 325
 DB 184 PNGQAKPSGARVP-----ISLVEQLSLAMHHTWYLATMFLFKDPVNMVLYFLV 234
 QY 326 HLVGGLLSHVYTFNHSYVEKFSALSSNMSYACLIQIMTRMRPGRFIDMLWGGLNYQI 385
 DB 235 QAVCGNLLAIYFSLNHGMPVISKEEAVDMDFTKQIITGRDVPGLFANFTGGLNYQI 294
 QY 386 EHLFPTMPRHNLNTVMPLVKEFAAANGPLVMYDDYFTGFWLEIEQFRNIANYAAKLTK 444
 DB 295 EHLFPTMPRHNFESKIQPAVETLCKKYNVRYHTTGMEGTAEVFSRLNEVSKAASKMGK 353

RESULT 5
 W84156
 ID W84156 standard; Protein: 746 AA.
 AC W84156;
 DT 15-FEB-1999 (first entry)
 DE Human desaturase enzyme encoded by contig 253538a.
 KW Fatty acid; desaturase; polyunsaturated fatty acid;
 KW malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis;
 KW cancer; diabetes; eczema; platelet aggregation; vasodilation;
 KW cholesterol level; endometriosis; premenstrual syndrome; human;
 KW myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;
 KW acute respiratory syndrome; hypertension; inflammatory skin disorder.

Result No.	Query	Score	Match	Length	DB	ID	Description
1	1	211	8.7	359	1	LLCD_SYN3	Q08871 synchocyst
2	1	165.5	6.8	387	1	FD61_SOYN3	Q48630 glycine max
3	3	142.5	5.9	383	1	FD6E_ARATH	P45313 arabidopsis
4	4	139.5	5.7	383	1	FD62_SOYNB	Q48631 glycine max
5	5	130.5	5.4	384	1	FD6E_BRAUJ	Q39287 brassica ju
6	1	129	5.3	351	1	DESA_SPIPL	Q54794 spirulina p
7	7	125	5.1	418	1	FD6C_ARATH	P46312 arabidopsis
8	8	124.5	5.1	351	1	DESA_SYN3	Q20388 synchocyst
9	9	120.5	4.9	443	1	FD6C_BRANA	P48627 brassica na
10	10	119.5	4.9	447	1	FD6C_SPIOL	P48629 spinacia ol
11	11	111	4.6	659	1	CR70_BACTO	P79693 bacillus th
12	12	108.5	4.5	442	1	YA17_SYN3	P72935 synchocyst
13	13	106	4.4	424	1	FD6C_SOYNB	P48628 glycine max
14	14	102.5	4.2	573	1	COX1_MYCTU	Q53290 mycobacteri
15	15	101	4.1	730	1	PSAB_SYN3	P29255 synchocyst
16	99	99	4.1	514	1	COX1_HALGR	P38595 halichoerus
17	98	98	4.0	380	1	FD3E_PHAAL	P32291 phaseolus a
18	96.5	96	4.0	487	1	GITT_ECOLI	P77405 escherichia
19	96	96	3.9	514	1	COX1_FELCA	P48888 felis silve
20	95	95	3.9	514	1	COX1_PHOVI	Q00527 phoca vitul
21	95	95	3.9	750	1	PSAA_ORISA	P12155 oryza sativ
22	95	95	3.9	432	1	YG3L_YEAST	P48236 saccharomyc
23	96	96	3.9	928	1	CHS2_EXODE	P30601 exophiala d
24	94	94	3.9	514	1	COX1_CANFA	Q92264 canis fami
25	94	94	3.9	513	1	COX1_DIDMA	P41310 didelphis m
26	94	94	3.9	259	1	COX3_ALBCO	P48891 albinaria c
27	92	92	3.9	732	1	PSAB_SYN2	P17155 synchococc
28	93	93	3.8	513	1	COX1_RABIT	P17155 synchococc
29	93	93	3.8	900	1	MANB_CAEGL	Q79429 oryctolagoc
30	92.5	92.5	3.8	751	1	PSAA_EUGER	Q93324 caenorhabdi
31	92	92	3.8	513	1	COX1_ORNAN	P19430 euglena gra
32	92	92	3.8	750	1	PSAA_TOBAC	Q36452 ornithorhyn
33	90.5	90.5	3.7	453	1	FD3C_SOYNB	P06405 nicotiana t
34	90.5	90.5	3.7	752	1	PSAA_MASLA	P48621 glycine max
35	90	90	3.7	513	1	COX1_MACRO	Q52474 macroglocl
36	90	90	3.7	383	1	FD32_BRANA	P92661 macrospor ro
37	90	90	3.7	380	1	FD3E_SOYNB	P48624 brassica na
38	90	90	3.7	379	1	FD3E_TOBAC	P48625 glycine max
39	89.5	89.5	3.7	320	1	CRTW_HAEPL	P48626 nicotiana t
39							Q39982 haematococ

310


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Db 134 LGHVEIHGDGAVRMSPEOHVG-----IYRFQFYIWGLYL-FIPFWFLYDYI 182
Qy 275 FVSQPTHYDY-----YRNTAYEOVGLSLHWAMSLGQLYFLPDMSTRIMFFLVSHLVGG 330
Db 183 LVLN-KGKYDHKIPFPQLEASLIGIKLLW---LGYVFGLP---LALGFSIPEVLIGA 235
Qy 331 -----FLSHVVTFNHYSVEKFASSNMSNACQIMTTRNMRPGR-FID 375
Db 236 SVTYMTGIWCTIFMLAHVLESTF-LTPDGESGAIDDEWAICQIRTTANFATNPFWN 294
Qy 376 WLGGLNLYQIEHLFTPMRHNLTVMPLVKEFAAANGLPYVDDYFTGF-----WLE 428
Db 295 WFCGGLNHQVTHFLFPNICHIIYPQLENIKQCBEGVEYKVPYPTFKAAIASNYRWLE 353

RESULT 2
ID FD61_SOYBN STANDARD; PRT; 387 AA.
AC P48630;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE OMEGA-6 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM ISOZYME 1
DE (EC 1.14.99.-).
GN FAD2-1.
OS Glycine (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae;
OC Glycine.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SEED.
RX MEDLINE; 96151506.
RA HEPPARD E.P., KINNEY A.J., STECCA K.L., MIAO G.H.;
RT "Developmental and growth temperature regulation of two different
RT microsomal omega-6 desaturase genes in soybeans.";
RL Plant Physiol. 110:311-319(1996).
CC -|- FUNCTION: ER (MICROSOMAL) OMEGA-6 FATTY ACID DESATURASE INTRODUCES
CC THE SECOND DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS.
CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
CC PHOSPHOLIPIDS.
CC -|- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -|- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
CC -|- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN DEVELOPING SEEDS.
CC -|- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/ OR BE INVOLVED IN METAL ION BINDING.
CC -|- SIMILARITY: TO OTHER PLANT ER OMEGA-6 FATTY ACID DESATURASES.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; L43920; AAB00859.1;
CC PFAM; PF00487; FA_desaturase; 2.
DR Oxidoreductase; Fatty acid biosynthesis; Endoplasmic reticulum;
KW Transmembrane.
FT TRANSMEM 54 74 POTENTIAL.
FT TRANSMEM 87 107 POTENTIAL.
FT TRANSMEM 121 141 POTENTIAL.
FT TRANSMEM 183 203 POTENTIAL.
FT TRANSMEM 227 247 POTENTIAL.
FT ANSMEH 251 271 POTENTIAL.
FT MAIN 109 113 HISTIDINE BOX 1.
FT IAIN 145 149 HISTIDINE BOX 2.
FT IAIN 319 323 HISTIDINE BOX 3.

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SQ SEQUENCE 387 AA; 44662 MW; 9F81BE96 CRC32;

Query Match 6.8%; Score 165.5; DB 1; Length 31
Best Local Similarity 23.3%; Pred. No. 1.7e-05;
Matches 88; Conservative 44; Mismatches 115; Indels 1

```

Qy 126 PLFYRKILET---ILETFAYLOYHTY---LP---SAILMGVAWOOLG--
Db 47 PICFQSLTSSYVYDLSFAFIYFIATYTHLLPQPSLIAMPYVWLOGCL.
Qy 170 I-HEFAHOLFKNRYND-----LASVYVGNFLOGFSSGGWKEQHNHHAATNVV 218
Db 107 IAECHGHAFSKYQWDDVVGVLTHSTLLVPYF-----SNKISHRRHHSNTGSL 155
Qy 219 GRDGDLDLVP--FYATVAEHLNYSQDSWNTLFRHQHWHWTMLPFLRLSLWLOSIFY 276
Db 156 DRDEVEVPKPSKVAWFSKYLNN-----PLGR-----AVSLVTLTIGWPMYLAFN 202
Qy 277 SQMP-----THYDY---YRN-----TAIYEOVGLSLHWAMSL-GOLYFLPDWST 317
Db 203 SGRPYDSFASHYHPYAPIYSNRRLIYVSDVALF-SVYSLYRVATLKGVLWLLCYGV 261
Qy 318 RIMFFFLVSHLVGGFLLSHVVTFNHYSVERFALSSNMSNACQIMTTRNMRPGRFIDWL 377
Db 262 PLL-----IVNGFL---VTITLQHTHEALPHYDSEW-----DWL 294
Qy 378 WGLG-----NYQIEHLFTPMRHN-----LNTVMPLVKEFAAANGLP 415
Db 295 KGAATMDRDYGLNKVFHHITDTHVAHLFTSMPHYHAMEATNAIKPILGEY----- 348
Qy 416 YMVDD--YFTGFWLEIEQ 431
Db 348 YQFDDTPFYKALWREARE 365

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RESULT 3

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ID FD6E_ARATH STANDARD; PRT; 383 AA.
AC P46313;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE OMEGA-6 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (EC 1.14.99.-)
DE (DELTA-12 DESATURASE).
GN FAD2.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
OC Arabidopsis.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 94176997.
RA OKULEY J., LIGHTNER J., FELDMANN K.A., YADAV N., LARK E., BROWSE J.;
RT "Arabidopsis FAD2 gene encodes the enzyme that is essential for
RT polyunsaturated lipid synthesis.";
RL Plant Cell 6:147-158(1994).
CC -|- FUNCTION: ER (MICROSOMAL) OMEGA-6 FATTY ACID DESATURASE INTRODUCES
CC THE SECOND DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS.
CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
CC PHOSPHOLIPIDS.
CC -|- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -|- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
CC -|- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/ OR BE INVOLVED IN METAL ION BINDING.
CC -|- SIMILARITY: TO OTHER PLANT ER OMEGA-6 FATTY ACID DESATURASES.
CC
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[1]
RN SEQUENCE FROM N.A.
RP MEDLINE: 92032774.
RA SMART L.B., MCINTOSH L.;
RT "Expression of photosynthesis genes in the cyanobacterium
RT Synechocystis sp. PCC 6803: psaa-psab and psba transcripts accumulate
RT in dark-grown cells.";
RL Plant Mol. Biol. 17:959-971(1991).
RN [2]
RN SEQUENCE FROM N.A.
RX MEDLINE: 97061201.
RA KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y.,
RA MIYAJIMA N., HIROSAWA M., SUGIURA M., SASAMOTO S., KIMURA T.,
RA OKUSUCHI T., MATSUNO A., MURAKI A., NAKAZAKI N., NARUO K.,
RA OKUMURA S., SHIMO S., TAKEUCHI C., WADA T., WATANABE A.,
RA YAMADA M., YASUDA M., TABATA S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
CC -!- FUNCTION: PSAA ALONG WITH PSAB BIND P700, THE PRIMARY ELECTRON
CC DONOR OF PHOTOSYSTEM I (PSI) AS WELL AS THE ELECTRON ACCEPTORS A0,
CC A1, AND FX.
CC -!- COFACTOR: P700 IS A CHLOROPHYL DIMER, A0 IS CHLOROPHYLL, A1 IS A
CC PHYLLOQUINONE AND FX IS A 4FE-4S IRON-SULFUR CENTER.
CC -!- SUBUNIT: HETERODIMER OF A1 AND A2 SUBUNITS WHICH BIND TOGETHER THE
CC IRON-SULFUR CENTER FX.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE PSAA/PSAB FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL: X58825; CA441630.1; -;
CC EMBL: D90906; BA417438.1; -;
CC PIR: S18243; S18243.
CC PIR: S19090; S19090.
CC PFAM: PF00223; psaa_psab; 1.
CC PROSITE: PS00419; PHOTOSYSTEM_I_PSAAB; 1.
CC Chlorophyll: photosystem I; Electron transport; Photosynthesis;
CC Transmembrane; Iron-sulfur; 4fe-4S.
CC
CC INIT_MET 0 BY SIMILARITY
CC FT TRANSMEM 45 68 I (POTENTIAL).
CC FT TRANSMEM 134 156 II (POTENTIAL).
CC FT TRANSMEM 174 198 III (POTENTIAL).
CC FT TRANSMEM 272 290 IV (POTENTIAL).
CC FT TRANSMEM 327 350 V (POTENTIAL).
CC FT TRANSMEM 366 392 VI (POTENTIAL).
CC FT TRANSMEM 414 436 VII (POTENTIAL).
CC FT TRANSMEM 513 531 VIII (POTENTIAL).
CC FT TRANSMEM 571 592 IX (POTENTIAL).
CC FT TRANSMEM 639 661 X (POTENTIAL).
CC FT TRANSMEM 703 723 XI (POTENTIAL).
CC FT METAL 555 555 IRON-SULFUR (4FE-4S).
CC FT METAL 564 564 IRON-SULFUR (4FE-4S).
CC FT CONFLICT 536 537 DA -> ES (IN REF. 1).
CC SEQUENCE 730 AA; 81160 MW; 7387ELAA CRC32;

Query Match 4.1%; Score 101; DB 1; Length 730;
Best Local Similarity 22.5%; Pred. No. 2.4;
Matches 89; Conservative 48; Mismatches 132; Indels 126; Gaps 24;
OY 26 VLRSHPGSAITYKNMADATVPHFTGSKAYQWLTKKCPQEPIDKDDPK 85
DB 45 IFASHFGHIAIIFL-WTSGTLFHVAVQGNFE--QWIKD-----PLNIRPIAHAIWDPHF 95
OY 86 GIDVNMGTFTNISEKRSAINKSFTDLRMVRAEGLDGSPLF---YIRKILETITILF 142

Db 96 GEGAVNAFT---QAGASNPVNIAYSGVYHWFYIIGTMTNQELYSAGAVELLVLSLF--LF 150
OY 143 AFYLOXYHTYPLPSAILMGVAVQOOLGWLIIHEFAHQLEKN---RYNDLASFYVGNFLQGE 199
Db 151 AGWLHLQPKFRPS-----LAW-----FKNAESRLNHHLAGLF-----GV 184
OY 200 SSGGWKEQHNVHAATNV---VGRDGLD-----LVPEYA-----TVAEHLN 238
Db 185 SSLAW-AGHLVHVAIPEARGQHVGDWDFLSTPPHPAGLMPFFTCGNWGVYAADPDAGHIF 243
OY 239 NYSODS-----WVMTLFRQHVHWTMLPFL-----RLSN-----LL 270
Db 244 GTSEGACTAILTFLGGFHPQTESLWLTDI---AHHLIAIAVIFIAGHMYRTNMGIGHSI 300
OY 271 QSIIFYSQMP-----THYYDYRNTAIYBQVGLSLHWMSLG-----QLYFLP--- 314
Db 301 KEILNAHKGPLTGAGHTNLYDTI--NNSLHFQLGLALA---SLGVITSLVAGHMYSLPSYA 356
OY 314 ----DMSRIMFPLVSHLVGGLLSHVVTENHYSV 344
Db 357 FIAQDHTTAAALYTHHQYIAGFLM--VGAFAGHAI 389

Search completed: February 24, 2000, 22:03:14
Job time: 16500 sec

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CC EMBL; AL021287; CAAL6128.1; -;
 CC DR PROSITE; PS00077; COX1; 1;
 CC DR PFAM; PF00115; COX1; 1;
 CC KW Oxidoreductase; Heme; Copper; Transmembrane; Respiratory chain.
 FT TRANSMEM 40 60
 FT TRANSMEM 89 109
 FT TRANSMEM 121 141
 FT TRANSMEM 170 190
 FT TRANSMEM 213 233
 FT TRANSMEM 258 278
 FT TRANSMEM 290 310
 FT TRANSMEM 315 335
 FT TRANSMEM 359 379
 FT TRANSMEM 398 418
 FT TRANSMEM 433 453
 FT TRANSMEM 476 496
 FT METAL 86 86
 FT METAL 264 284
 FT METAL 268 288
 FT METAL 313 313
 FT METAL 314 314
 FT METAL 397 397
 FT METAL 399 399
 SQ SEQUENCE 573 AA; 63672 MW; 79C8326 CRC32;

Query Match 4.2%; Score 102.5; DB 1; Length 573;
 Best Local Similarity 21.8%; Pred. No. 1.4;
 Matches 89; Conservative 49; Mismatches 115; Indels 155; Gaps 25;

QY 116 VRAEGL-MDGSPLFYKIRKILETITLFAFYQYHTYVLPSSAILMGVA----- 163
 DB 196 MRAPGTMERMPF-TWNIWVTSILILIAFPLL-----TAALFGLAADRHLAGHIYDA 247
 QY 163 -----WQQLGWLIIHEFAHQLF-----KRRYNDLASVYGVGNFLQ 197
 DB 248 ANGVLMLWOLF-----FGHPEYIIALPFGIVSEIFVFSRKPFGYTLTVATLSIA 304
 QY 198 GFSSGGWKEQHNVHHA-ATNVVGRDGLDLPVFA-----TVAEHLNYSQDSWVM 247
 DB 305 ALSAVM-----AHHMFATGAV-----LLPFSFTYLIATVGTGKFFN-----WIG 346
 QY 248 TLFRRWQHWHVT-----FMLPFLRLSWLLQSIIFVSQMPHYDYIYRNTAIYEQV----- 297
 DB 347 TMMKGQLTFTFPMFLFSVGFVMTFL-LGLATGVLLASPLDFHVTDSYFVVAHFHVLFGT 405
 QY 297 -----GLSLHNAW-----SLGQLYFLPDWSTIRMF---FLVSHLVG----- 330
 DB 406 IVFATFAGI---YFWFPEKMTGRLLDERLGLHF---WLTFTGFTTFLVQHWLGDGMPR 459
 QY 330 -----GFLLSHVVTENHYSVEKFAISS-----NIMSNVACIQIMTRNMRPGR 373
 DB 460 RYADLPDQFQGLNVVS-----TIGAFILGASMEFPFVNVKFSWRYGEVVI----- 507
 QY 374 IDMLWGLNTQIEHLLPPTPRHNLNTVPLVKFAAANGI--PYMVD 419
 DB 507 VDPWGYGN-SLEWATSCPPRRNF-TLPRIASERPAFELHYPHMVE 552

RESULT 15
 PSAB_SYN3
 ID PSAB_SYN3 STANDARD; PRT; 730 AA.
 AC P29255; P73398;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE PHOTOSYSTEM I P700 CHLOROPHYLL A APOPROTEIN A2.
 GN PSAB OR SLR1835.
 OS Synechocystis sp. (strain PCC 6803).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.

QY 158 LMGVAWQQLGLI-----HEFAHQLFKNRYNDLASVYGVGNFL---QGFSGGWKEQ 207
 DB 145 LLPLAVWVTGTAITGFVIGHDCAHRSFSGKLVEDI-----VGTAFMPLIYIYEPWREK 200
 QY 208 HNVHHAATNVVGRD-----GDLVPPYATVAEHLNYSQDSWMTFLRQHVHWT 259
 DB 201 HNRHAKTNMLREDTAWHPWKDEPSTPLLRKAI--IYCYGPFRCWMSIAHW--LWVHF 256
 QY 260 MLPFLRLSWLLQSIIFVSQMPHYDYIYRNTAIYEQVGLSLHNAWSLQGL-YELPDWSTR 318
 DB 257 DLKKFR-----PSEVP-----RVKISLACVFAFIAIGVPLLIYKGT 292
 QY 319 IM-----FFLVSHLVGFLLSHVVTENHYSVEKFAISSNIMSNVACIQIMTRNMRPGRFI 374
 DB 293 IINGWIKFWMPLWGLYHFWMS-TFTMVHTTAPYIPFYISEENRAQAQLNGTVHCDYPKWI 351
 QY 375 DNLWGLNLYQIEHLLPPTPRHNLNTVPLVKE 407
 DB 352 EILCHDINVHIPHISPRIPSYNLRAHKSQZ 384

RESULT 14
 COX1_MYCTU
 ID COX1_MYCTU STANDARD; PRT; 573 AA.
 AC O53290;
 DT 15-DEC-1999 (Rel. 39, Created)
 DT 15-DEC-1999 (Rel. 39, Last sequence update)
 DT 15-DEC-1999 (Rel. 39, Last annotation update)
 DE PROBABLE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (CYTOCHROME A3 SUBUNIT 1).
 DE A3 SUBUNIT 1).
 GN CTAD OR RV3043C OR MTV012.58C.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-H37RV;
 RX MEDLINE; 98295987.
 RA COLE S.T., BROSC R., PARKHILL J., GARNIER T., CHURCHER C., HARRIS D.,
 RA GORDON S.V., EIGLMEIER K., GAS S., BARRY C.E. III, TEKAIA F.,
 RA BADCOCK K., BASHAM D., BROWN D., CHILLINGWORTH T., CONNOR R.,
 RA DAVIES R., DEVLIN K., FETWELL T., GENTLES S., HAMLIN N., HOLROYD S.,
 RA HORNSBY T., JAGELS K., KROGH A., MCLEAN J., MOULE S., MORPHY L.,
 RA OLIVER S., OSBORNE J., QUAIL M.A., RAJANDREAM M.A., ROGERS J.,
 RA RUTTER S., SEEGER K., SKELTON S., SQUARES S., SQUARES R., SULSTON J.E.,
 RA TAYLOR K., WHITEHEAD S., BARRELL B.G.;
 RT "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."
 RL Nature 393:537-544 (1998).
 CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNIT 1-3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. CO I IS THE CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3 AND COPPER B (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4 FERRICYTOCHROME C.
 CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
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OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
 OC core eudicots; Caryophyllales; Caryophyllaceae; Chenopodiaceae;
 OC Spinacia.
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 66-78.
 RC STRAIN=CV. SUBITO; TISSUE=LEAF;
 RX MEDLINE: 95036044.
 RA SCHMIDT H., DRESSLERHAUS T., BUCK F., HEINZ E.;
 RT "Purification and PCR-based cDNA cloning of a plastidial n-6
 RL Plant Mol. Biol. 26:631-642(1994).
 CC -|- FUNCTION: CHLOROPLAST OMEGA-6 FATTY ACID DESATURASE INTRODUCES
 CC THE SECOND DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY
 CC ACIDS, IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT
 CC TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
 CC ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.
 CC -|- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
 CC -|- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).
 CC -|- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
 CC AND/OR BE INVOLVED IN METAL ION BINDING.
 CC -|- SIMILARITY: TO OTHER PLANT CHLOROPLAST OMEGA-6 FATTY ACID
 CC DESATURASES.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X78311; CAAS5121.1; ..
 DR PFAM: PF00487; FA_desaturase; 1.
 KW Oxidoreductase; Fatty acid biosynthesis; Chloroplast; Membrane;
 KW Transit peptide.
 FT TRANSIT 1 65 CHLOROPLAST.
 FT CHAIN 66 447 OMEGA-6 FATTY ACID DESATURASE.
 FT DOMAIN 171 175 HISTIDINE BOX 1.
 FT DOMAIN 207 211 HISTIDINE BOX 2.
 FT DOMAIN 367 371 HISTIDINE BOX 3.
 SQ SEQUENCE 447 AA; 51306 MW; 7C569B1E CRC32;
 Query Match 4.9%; Score 119.5; DB 1; Length 447;
 Best Local Similarity 21.8%; Pred. No. 0.056;
 Matches 71; Conservative 38; Mismatches 113; Indels 103; Gaps 15;
 QY 124 GSPLEFVIRKILETIFILFAFYLYQHYLYPLSAILMGVAQQLGWLII-----HEFAHH 176
 DB 128 GTVLISVTSVALGIFIAKAPV-----YLLP-----LAWWTGTAITGFFVIGHDCAHK 176
 QY 177 QLFKNRYNDLASYFVGNEL---QGSSGGWKEQHNVHHAATNVVGRD-----GDLD 225
 DB 177 SFSKNLVEDI-----VCTLAFLPLIYPYEPFRKDHQHTKTNMLREDTAWLPIMKEDIE 232
 QY 226 LVP-----FYATVAEHLNNYSODSWNTLFRMOHVHTF-----MLP 262
 DB 233 SSPGLRKALIYA-----YGLRTWMSIAHLKVFHFNELKDFRQSEVKRATISLAAVFA 284
 QY 263 FLRLSLQSLIFVSQMPHYDYRYNTAIYEQVLSLHAWSLGQLYFLPDKSTRIMEF 322
 DB 285 FMVIGMPL---IIY-----KTGI---VG-----N---IKFW 306
 QY 323 LVSHLVGGFLSHVHTFNHYSVEKFALSSNIMSYACLOIQTMTNRMPGRFIDWLWGLN 382
 DB 307 LMPWLCYHFWMS--TFTIVHHTAHPHPKSKENNAQAQLSGIVCHCDYPRWIELCHDIS 365
 QY 383 YQIEHFLFTPTMPRHNLNTVNLVKE 407
 DB 366 VHPHPHISPKIPSYNLRANQSLNE 390
 RESULT 11

CR70_BACTO STANDARD; PRT; 659 AA.
 ID CR70_BACTO
 AC F1789;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE 75 KD CRYSTAL PROTEIN (DELTA ENDOTOXIN).
 GN CRYIIIB.
 OS Bacillus thuringiensis (subsp. tolworthi).
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Bacillus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=43F;
 RX MEDLINE: 90206811.
 RA SICK A., GAERTNER F.H., WONG A.;
 RT "Nucleotide sequence of a coleopteran-active toxin gene from a new
 RT isolate of Bacillus thuringiensis subsp. tolworthi.";
 RL Nucleic Acids Res. 18:1305-1305(1990).
 CC -|- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
 CC EPITHELIAL CELLS OF COLEOPTERA.
 CC -|- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
 CC SPOROULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
 CC OF THE SPORE COAT.
 CC -|- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
 CC N-TERMINUS.
 CC -|- SIMILARITY: 69% IDENTITY TO THE 70 KD CRYSTAL PROTEIN OF STRAIN
 CC TENEBRIONIS (AC P07130).
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X17123; CAAS4983.1; ..
 DR EMBL: A07234; CAAC0645.1; ..
 DR PIR: S10228; S10228.
 DR HSSP: P07130; 1DLC.
 DR PFAM: PF00555; endotoxin; 1.
 KW Toxin; Sporulation.
 SQ SEQUENCE 659 AA; 75159 MW; 218F75C3 CRC32;
 Query Match 4.6%; Score 111; DB 1; Length 659;
 Best Local Similarity 20.7%; Pred. No. 0.38;
 Matches 95; Conservative 49; Mismatches 185; Indels 130; Gaps 19;
 QY 81 DDPKIGIDDVNMGTNFISEKRSR-QINKSFTDLRMVRAEGLMDGSPFYIRKILETIFT 139
 DB 150 EDVYNALDSKKAPVNLRSRRSQDRIRLEFSQAESHFR-----NSMPSFAVSK-FEVLFL 203
 QY 140 ILFAFYLYQHYTYPLPSAILMGVAQQLGWLIIHEFAHHQFLKNRYND--LASYFVG-NFL 196
 DB 204 PTYAQAANTHLLLLKDAQVEGEWYSSSEDIAEFYQQLKTOQYDHCNVNMYVGNLSL 263
 QY 197 QGSSGGWKEQHNVHHAATNVVGRDGLDV---PFVAT-----VAEHLNNYSQDSWVM 247
 DB 264 RGSTYDAWKFNFRREMTLTV-----LDLIVLFPFDVRLYKGVKVTELTRDITDPIF 318
 QY 248 TLFRRQHVHTFMFLPFLRLSWLLQSIFFVSQMPHYDYRYNTAIYEQV--GLS-----L 300
 DB 319 TLNALQYEGPTF-----SSSENSIRKPHLFDYLRGIEFHTLRPGYSGKDSFN 366
 QY 301 HWANSL-----GOLYFLPDWSTRIMFLVSHLV 328
 DB 367 YWSGNTVETRPSIGSNDTITSPFYGDKSIEPIQKLSFDGKVYRTIANTDIAAFPDKIY 426
 QY 329 GGFLLSHVHTFNHYSVEKFALSSNIMS-----KVDYSDQDKNETSTQTYDSKRYNGVLGAQDSIDQLPETTDEPLEKAYSHQ 483

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DR EMBL; D90912; BAAL18169.1; --
DR PIR; S11519; S11519.
DR PROSITE; P500374; FATTY_ACID_DESATUR_2; 1.
DR PFAM; PF00487; FA_desaturase; 1.
FT DOMAIN 90 94 HISTIDINE BOX 1.
FT DOMAIN 126 130 HISTIDINE BOX 2.
FT DOMAIN 287 291 HISTIDINE BOX 3.
SQ SEQUENCE 351 AA; 40495 MW; 9417790 CRC32;

Query Match
Best Local Similarity 5.1%; Score 124.5; DB 1; Length 351;
Matches 80; Conservative 55; Mismatches 159; Indels 93; Gaps 16;

QY 70 PTQEPPIKDDPIKIDVNGTNTSEKRAQINKSFDTLRLMRVRAEGLMDGSPLFY 129
D 10 PTWPSNPDRPIADKLQDIKLPKECFEKASKAWAS----- 49
QY 130 IRKILETIFTLFAF---YLOHTYLYPSAILMGVAWQOLGWL-----HEFAHQH 178
D 49 ---VLITLGAIVGILYLPW---YCLP-----ITWITGALTGAFFVGHDCGHRSF 97
QY 179 FKNRYNDLASFYV-GNFGQSSGGWKQHNHHAATNVVGRDGLD---LVPFYATVA 234
D 98 AKRWVNDLVGHAFAPLIYPFHS--WRLLDHHLHHTKNKIEVDNANDPMSVEAFQASPA 155
QY 235 EHLNNYSODS---WYMTLFRQHVHTFMLPELRLSWLQSIIFVSQMPHYDYRNT 290
D 156 IVRLFYRAIRGPFWMTGSIFPHSLMHFKL-----SNEAQRDRN- 194
QY 291 AIYEQVGLSHWANSGLQLYF-----LPDWSTRIMFFLVSHLVGGFLLSHVVTFNHSV 344
D 194 ----KVLSIAVVLEFAATFAFPAIITGVNGF-VKFWLMPWLVYHFWS-TFTIVHHTI 247
QY 345 EKFASSNMSNVACQIQTTRNMRCRFDLWGLGNTQIEHHLFPTMPRHNLVMP 404
D 248 PEIRFPAADWSAAEAQLNGTVHCDYPRWVEVLCHDINVHIPHLSVAIPSYNLRHAGS 307
QY 405 VKEFAANGLPYVDDYFTGFWLEIQ 431
D 308 LKE----NWGPFYERTFN--WOLMQ 328

RESULT 9
FD6C_BRANA STANDARD; PRT; 443 AA.
AC P48627;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DE OMEGA-6 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR (EC 1.14.99.-).
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Rosidae; eucosids II; Brassicales; Brassicaceae;
OC Brassica.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SEED;
RX MEDLINE; 94345008.
RA HITZ W.D., CARLSON T.J., BOOTH J.R. JR., KINNEY A.J., STECCA K.L.,
RA YADAV N.S.;
RT "Cloning of a higher-plant plastid omega-6 fatty acid desaturase cDNA
RT and its expression in a cyanobacterium.";
RL Plant Physiol. 105:635-641(1994).
CC -1- FUNCTION: CHLOROPLAST OMEGA-6 FATTY ACID DESATURASE INTRODUCES
CC THE SECOND DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY
CC ACIDS, IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT
CC TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).

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CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: TO OTHER PLANT CHLOROPLAST OMEGA-6 FATTY ACID
CC DESATURASES.

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CC or send an email to license@sib-sib.ch).

CC EMBL; L29214; AAA50157.1; -
CC PFAM; PF00487; FA_desaturase; 1.
CC Oxidoreductase; Fatty acid biosynthesis; Chloroplast; Membrane;
CC Transit peptide.
CC TRANSIT 1 64 CHLOROPLAST (BY SIMILARITY).
CC CHAIN 65 443 OMEGA-6 FATTY ACID DESATURASE.
CC DOMAIN 166 170 HISTIDINE BOX 1.
CC DOMAIN 202 206 HISTIDINE BOX 2.
CC DOMAIN 362 366 HISTIDINE BOX 3.
CC SEQUENCE 443 AA; 50755 MW; C814102A CRC32;

Query Match 4.9%; Score 120.5; DB 1; Length 443;
Best Local Similarity 19.5%; Pred. No. 0.04;
Matches 83; Conservative 62; Mismatches 140; Indels 141; Gaps 20;

QY 67 KECTPEIPDKDDP---IKGIDVNG---TFNISEKR----- 102
D 16 QOCLPAPKLASARLSPGVAVRPIDLLKGRTRTLVPAKKRIGIKAVFVPVAPSAD 75
QY 102 ---SAQINKSF---TDLRMVRAEGLMDGSP--LFYI-----RKILETIFTLFA 143
D 76 NAEDREQLAESYGFKGIGQDLPDNLTKDIMDTLPKEVEIDDDVKAWSVLISVTSYALG 135
QY 144 FYL--QYHTYLYPSAILMGVAWQOLGWL-----HEFAHQHOLFKNRYNDLASFVGN 194
D 136 LFMIKAPWYLLP-----LAWAWTGTAVTGFFVIGHDCAHKSFKNKLVEDI---VGT 185
QY 195 --FLQ-GFSSGGWKQHNHHAATNVVGRDGLDLPFYATVAEHLNN-----Y 240
D 186 LAFPLVLYPEWRFKHDRHAKTNMLVHDTAQVPP-----PEEDSSPVLKRIIFY 240
QY 241 SODSWMTLFRQHVHTFML-----PFLRLSWLQSIIFVSOMPT 281
D 241 GPTRPWLSTAHW--VNHENLRKFRPSEVNRVKISLACVFAFMAVGWPL----- 288
QY 282 HYDYRYNTAIYEOVGLSHWANSGLQLYFLPDWSTRIMFFLVSHLVGGFLLSHVVTFNH 341
D 288 -----ITYKGV-LGW-----VKFWLMPWLVYHFWS-TFTMVH 319
QY 342 YSVKFASSNMSNVACQIQTTRNMRCRFDLWGLGNTQIEHHLFPTMPRHNLTV 401
D 320 HTAPHFPFPADEWNAQAQLNGTVHCDYPSWIEILCHDINVHIPHISPRIPSYNLRRA 379
QY 402 MPLVKE 407
D 380 HQSIOE 385

RESULT 10
FD6C_SPIOL STANDARD; PRT; 447 AA.
ID FD6C_SPIOL
AC P48629;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE OMEGA-6 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR (EC 1.14.99.-).
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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Db 143 ---PWRKEEYQAGKFMQVT-----YDLFRGAWW--IGSILWA----- 178
Qy 308 QLYFLPDWS-----TRIM-----FFLVSHLVGGFL 332
Db 178 SIHF--DWTKEGKQKQVKESSLLVIGAAIAFTMTLIGVWGPFVKWIPWLFVHEW 235
Qy 333 LSHVTVFNHYSVEKALSSNMSNVACIQIMTRNRPGRFDLWLGGLNYQIEHHLFT 392
Db 236 MS-TFTLLHTTIADIPREPEQWHEAESQSGTVHCHNSYRWGEFLCHDINVHPHVTTA 294
Qy 393 WPHNLNTVMPVLKE 407
Db 295 IPWYNLRTPTPVYRK 309

RESULT 7
FD6C_ARATH STANDARD; PRT; 418 AA.
AC P46312;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE OMEGA-6 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR (EC 1.14.99.-).
GN FAD6 OR FADC.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC eumyllophytes; Spermatophyta; Magnoliophyta; Eudicotyledons;
OC core eudicots; Rosidae; eucots II; Brassicales; Brassicaceae;
OC Arabidopsis.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. COLUMBIA;
RA FALCONE D.L., GIBSON S., LEMIEUX B., SOMERVILLE C.R.;
RT "Identification of a gene that complements an Arabidopsis mutant
RT deficient in chloroplast omega 6 desaturase activity.";
RL Plant Physiol. 106:1453-1459(1994).
CC -1- FUNCTION: CHLOROPLAST OMEGA-6 FATTY ACID DESATURASE INTRODUCES
CC THE SECOND DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY
CC ACIDS, IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT
CC TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).
CC -1- DEVELOPMENTAL STAGE: HIGHEST LEVELS FOUND IN EXPANDING LEAVES.
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/ OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: TO OTHER PLANT CHLOROPLAST OMEGA-6 FATTY ACID
CC DESATURASES.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: U09503; AAA92800.1;
CC PFAM: PF00487; FA_desaturase; 1.
CC Oxidoreductase; fatty acid biosynthesis; Chloroplast; Membrane;
CC Transit peptide.
FT TRANSIT 1 69 CHLOROPLAST (BY SIMILARITY).
FT CHAIN 70 418 OMEGA-6 FATTY ACID DESATURASE.
FT DOMAIN 171 175 HISTIDINE BOX 1.
FT DOMAIN 207 211 HISTIDINE BOX 2.
FT DOMAIN 367 371 HISTIDINE BOX 3.
FT SEQUENCE 418 AA; 47729 MW; C4700789 CRC32;
SQ

Query Match 5.1%; Score 125; DB 1; Length 418;
Best Local Similarity 21.7%; Pred. No. 0.02;

```

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Matches 73; Conservative 47; Mismatches 132; Indels 84; Gaps 14;
Qy 111 DLRMVRVREGLMDGSP--LFYI--RKILETIFILFAFYLOYHTYVLPSSAILMGVAWQOL 166
Db 100 DLPEVNTLKDINDTPKEVFEIDDLKALKSVLSVTSYTLGLPMIAKSPWYLLPLAWMT 159
Qy 167 GWLI-----HEFAHQFLFKNRYNDLASIFYGN--FLQ-GFSSGGKQKHQVHVHAATN 216
Db 160 GTAITGFFVIGHDCAKHSKKNLVEDI---VGTIAFLPLVYPYEPWREKHDRHAKTN 215
Qy 217 VVGRDGLDLVP---FYATVAEH---LNNYSQDSWVMTLFRHWHVHTFML----- 262
Db 216 MLVHDTAWQVPPEEPESPVMRKAIIFGVGPIRPWLSIAHW--VNMHFNKKFRASEVN 273
Qy 262 -----PELRLSWLLOSIIFVSOMPTHYYDYRNATYIYEQVGLSLHWANSLGOLYF 311
Db 274 RVKISLACVFAFMAVGWPL-----IVYKGI-LGM----- 303
Qy 312 LPDWSTRIMFFVLSHLVGGFLLSHVVTENHYSVEKFALSSNMSNVACIQIMTRNMRPG 371
Db 303 -----VWFMLMPWLGCFHWMS-TFTVHHTAPHIPFRPADEWNAQAOLNGTVHCDYP 354
Qy 372 RFIDWLWGLNGVQIEHHLFTPMRPNLNTVMPVLKE 407
Db 355 SWIEILCHDINVPHHISPRIPSYNLRRAAHSIQE 390

RESULT 8
DESA_SYNY3
ID DESA_SYNY3 STANDARD; PRT; 351 AA.
AC P20388;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 13-DEC-1998 (Rel. 37, Last annotation update)
DE FATTY ACID DESATURASE (EC 1.14.99.-) (DELTA 12 DESATURASE).
GN DESA OR SLR1350.
OS Synecocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synecocystis.
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE; 90370121.
RA WADA H., GOMBOS Z., MURATA N.;
RT "Enhancement of chilling tolerance of a cyanobacterium by genetic
RT manipulation of fatty acid desaturation.";
RL Nature 347:200-203(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC MEDLINE; 97061201.
RA KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y.,
RA MIYAJIMA N., HIROSAWA M., SUGIURA M., SASAMOTO S., KIMURA T.,
RA HOSOUCHI T., MATSUNO A., MURAKI A., NAKAZAKI N., NARUO K.,
RA OKUMURA S., SHIMPO S., TAKEUCHI C., WADA T., WATANABE A.,
RA YAMADA M., YASUDA M., TABATA S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synecocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
CC -1- FUNCTION: CAN INTRODUCE A SECOND CIS DOUBLE BOND AT THE DELTA 12
CC POSITION OF FATTY ACID BOUND TO MEMBRANE GLYCEROLIPIDS. THIS
CC ENZYME IS INVOLVED IN CHILLING TOLERANCE BECAUSE THE PHASE
CC TRANSITION TEMPERATURE OF LIPIDS OF CELLULAR MEMBRANES DEPENDS ON
CC THE DEGREE OF UNSATURATION OF FATTY ACIDS OF THE MEMBRANE LIPIDS.
CC -1- SIMILARITY: TO PLANTS STEAROYL-ACP DESATURASE.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: X53508; CAA37584.1;
CC
CC DR

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Db 128 SFLLVPYFS---WKYSHRRHHSSNTGSLERDEVFPVKKKSD---IKWY---GKYLNNPIGR 178

[illegible]

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Query Match      5.3%; Score 129; DB 1; Length 351;
Best Local Similarity 19.0%; Pred. No. 0.0083;
Matches 60; Conservative 50; Mismatches 87; Indels 118; Gaps

QY 155 SAILMGVAWQQLG---WLI-----HEFAHHOLFKNRYNDLASVYF 192
      : : : | : | : | : | : | : | : | : | : | : | : |
Db 51 NVVMVGLGWIATAPWFLLPVVMVFTGALTGFVIGCHGHRFSRNWVND---wV 106

QY 193 GNFL-----QGFSSGGWEQHNVHAAANVYVGRGDLDLPFYATVAEHLNYSODSWVM 247
      ||| | | | | | | | | | | | | | | | | | : | : |
Db 107 GHILFLPIYPHPS--WRIGHQNHKYNRM-----ELD-----NAWQ-- 143

QY 248 TLFRRQHVHTFMFLPFLRLSLMLQSTIEFVSOMPTHYDYRNTATIEOVGLSLHWAMSLG 307

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CC DNA are used as probes to isolate related coding sequences. Recombinant plants can produce high yields of PUFA, since new pathways can be created and unwanted ones suppressed. Plants can be engineered to express oils of particular PUFA composition, e.g. one similar to that in human milk, and product recovery is simpler than with e.g. fish.

CC Sequence 457 AA;

Query Match 25.8%; Score 629; DB 1; Length 457;
 Best Local Similarity 33.0%; Pred. No. 1.2e-56;
 Matches 154; Conservative 76; Mismatches 175; Indels 13;

QY 4 RQEEHEPFPIKIDGKWCQIDDAVLRSHPGSGSAITTKYKNNDAITVFTFTGSKAEQWLT 63
 DB 25 KDAEAPFLMIDNKVDVRETV-PDHGSGSVILTHVGKGDVDFDTH---PEA-AWET 79
 QY 64 ELKCEPTQEPPIKIDGKWCQIDDAVLRSHPGSGSAITTKYKNNDAITVFTFTGSKAEQWLT 123
 DB 80 LANFVVGDIIDSDRDKNDF-----AAEVRK-----LRTLFQSLGYD 118
 QY 124 GSPFYIRKI-----LETFTILFAFYLOHYTY-YLPSSAILMGVAQOGLWLIHFAHQ 177
 DB 119 SSKAYTAFKVSFNLGSLTIVAKGQTSITLANVLSAALGLFWQCGWLAHDFLHQ 178
 QY 178 LFKNRYNDLASFYFVGNFQSGGKQHNHVAATNVVGRDGLDLPVFAVAEHL 237
 DB 179 VFQDRFWGLDFAFLGCVGCGFSSSWKDKHNTTHAHPNVHGEDPDIDHPL-LTWSEHA 237
 QY 238 NNYSOD-----SWMTLFRQVHHTF--MLPFLRLSWLLQSIIFV-----SQ 278
 DB 238 LEWSDVPDEELTRMWSRPMVNLQTFYFPLSFARLSWCLQSILFVLPNGOAHKPSGAR 297
 QY 279 MPTHYDIYRNTAIYEOVGLSHWASLGQLY-FLPDWSTRIMFVLSHVLGFLSHVV 337
 DB 298 VP-----ISLVEQLSLAMHWTYLATMELFKDPVNMVLYFLVSAVCGNLLAIF 348
 QY 338 TFNHSYVERKALSSNMSNVACLOIMTTRNMRPGRIDWLWGLNLYQIEHHLPFTMPRN 397
 DB 349 SLNHGMPVISKEEAVDMDFFTKQITGRDVHPGLFANWFTGGLNLYQIEHHLPFTMPRN 408
 QY 398 LNTVMPLKEFAAANGPLVMYDDYFTGFWLEIEQFNRNIANAAKLT 444
 DB 409 FSKIQPAVETLCKKYNRYHTTGMIEGTAEVFSRLNEVSKAASKMGK 455

RESULT 3
 W85121
 ID W85121 standard; peptide: 457 AA.
 DE 11-FEB-1999 (first entry)
 KW Fatty acid; delta-6 desaturase; polyunsaturated fatty acid;
 KW malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis;
 KW cancer; diabetes; eczema; platelet aggregation; vasodilation;
 KW cholesterol level; endometriosis; premenstrual syndrome;
 KW myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;
 KW acute respiratory syndrome; hypertension; inflammatory skin disorder.
 OS Unidentified.
 PN W09846765-A1.
 PD 22-OCT-1998.
 PR 10-APR-1998; U07421.
 PR 11-APR-1997; US-833610.
 PR (ABBO) ABBOTT LAB.
 PA (CALJ) CALGENE LLC.
 PI Chaudhary S, Huang Y, Knutson D, Leonard AE, Mukerji P, Thurmond J.
 DR WPI: 99-009334/01.
 PT New nucleic acid encoding delta5 and other desaturase enzymes .
 PT useful in production of oils of increased arachidonic acid content,
 PT used, e.g. for treating cancer, as foods, animal feeds and cosmetics
 PS disclosure; pages 95-96; 153pp; English.
 CC The present sequence represents a fatty acid delta-6 desaturase enzyme.
 CC The specification describes methods for desaturating a fatty acid and

QY 124 GSPFYIRKI-----LETFTILFAFYLOHYTY-YLPSSAILMGVAQOGLWLIHFAHQ 177
 DB 119 SSKAYTAFKVSFNLGSLTIVAKGQTSITLANVLSAALGLFWQCGWLAHDFLHQ 178
 QY 178 LFKNRYNDLASFYFVGNFQSGGKQHNHVAATNVVGRDGLDLPVFAVAEHL 237
 DB 179 VFQDRFWGLDFAFLGCVGCGFSSSWKDKHNTTHAHPNVHGEDPDIDHPL-LTWSEHA 237
 QY 238 NNYSOD-----SWMTLFRQVHHTF--MLPFLRLSWLLQSIIFV-----SQ 278
 DB 238 LEWSDVPDEELTRMWSRPMVNLQTFYFPLSFARLSWCLQSILFVLPNGOAHKPSGAR 297
 QY 279 MPTHYDIYRNTAIYEOVGLSHWASLGQLY-FLPDWSTRIMFVLSHVLGFLSHVV 337
 DB 298 VP-----ISLVEQLSLAMHWTYLATMELFKDPVNMVLYFLVSAVCGNLLAIF 348
 QY 338 TFNHSYVERKALSSNMSNVACLOIMTTRNMRPGRIDWLWGLNLYQIEHHLPFTMPRN 397
 DB 349 SLNHGMPVISKEEAVDMDFFTKQITGRDVHPGLFANWFTGGLNLYQIEHHLPFTMPRN 408
 QY 398 LNTVMPLKEFAAANGPLVMYDDYFTGFWLEIEQFNRNIANAAKLT 444
 DB 409 FSKIQPAVETLCKKYNRYHTTGMIEGTAEVFSRLNEVSKAASKMGK 455

RESULT 2
 W95504
 ID W95504 standard; peptide: 457 AA.
 DE 26-MAR-1999 (first entry)
 KW Mortierella alpina delta 6 desaturase.
 KW delta 6 desaturase; recombinant; fatty acid desaturase; FAD; PUFA; oil;
 KW polyunsaturated fatty acid; linoleic acid; arachidonic acid; linolenic;
 KW stearidonic acid; eicosapentaenoic acid; malnutrition; feeding formula;
 KW dietary supplement; prostaglandin; restenosis; angioplasty; inflammation;
 KW rheumatoid arthritis; psoriasis; osteoporosis; cancer; eczema; AIDS;
 KW diabetes; cosmetic; animal feed.
 OS Mortierella alpina.
 PN W09846764-A1.
 PD 22-OCT-1998.
 PR 10-APR-1998; U07421.
 PR 24-OCT-1997; US-956985.
 PR 11-APR-1997; US-833610.
 PR 11-APR-1997; US-834033.
 PR 11-APR-1997; US-834655.
 PA (ABBO) ABBOTT LAB.
 PA (CALJ) CALGENE LLC.
 PI Chaudhary S, Huang Y, Knutson D, Leonard AE, Mukerji P, Thurmond J.
 DR WPI: 99-080739/07.
 DR N-PSDB: X00889.
 PT Nucleic acid construct able to express fatty acid desaturase in
 PT plants - useful in human or animal nutrition, as cosmetics and
 PT therapeutically, e.g. for restenosis, cancer and diabetes
 PS Claim 7; Fig 3A-E; 210pp; English.
 CC This represents a Mortierella alpina delta 6 desaturase. The invention
 CC relates to a nucleic acid construct that contains at least one of the
 CC nucleotide sequences (X00889 to X00891) encoding M. alpina delta 6,
 CC delta 12 and delta 5 desaturases (W95504 to W95506) respectively, coupled
 CC to an expression control sequence functional in plants. Recombinant plant
 CC cells containing at least one DNA encoding a M. alpina fatty acid
 CC desaturase (FAD), can be used for the production of polyunsaturated fatty
 CC acid (PUFA). These recombinant cells or plants containing them are used
 CC to produce oils such as linoleic acid, arachidonic acid, gamma-linolenic
 CC acid, dihomogamma-linolenic acid, stearidonic acid and eicosapentaenoic
 CC acid (EPA). These plant oils are used: (i) to treat malnutrition; (ii) in
 CC infant feeding formulas, or dietary supplements or substitutes, for use
 CC in humans or animals; (iii) for treating disorders associated with
 CC inadequate consumption or production of PUFA (or their metabolites such
 CC as prostaglandins), e.g. restenosis after angioplasty, inflammation,
 CC AIDS, rheumatoid arthritis, psoriasis, osteoporosis, cancer, eczema,
 CC diabetes; (iv) as cosmetics, and (v) as animal feeds. Fragments of the

CC DNA are used as probes to isolate related coding sequences. Recombinant plants can produce high yields of PUFA, since new pathways can be created and unwanted ones suppressed. Plants can be engineered to express oils of particular PUFA composition, e.g. one similar to that in human milk, and product recovery is simpler than with e.g. fish.

CC Sequence 457 AA;

Query Match 25.8%; Score 629; DB 1; Length 457;
 Best Local Similarity 33.0%; Pred. No. 1.2e-56;
 Matches 154; Conservative 76; Mismatches 175; Indels 13;

QY 4 RQEEHEPFPIKIDGKWCQIDDAVLRSHPGSGSAITTKYKNNDAITVFTFTGSKAEQWLT 63
 DB 25 KDAEAPFLMIDNKVDVRETV-PDHGSGSVILTHVGKGDVDFDTH---PEA-AWET 79
 QY 64 ELKCEPTQEPPIKIDGKWCQIDDAVLRSHPGSGSAITTKYKNNDAITVFTFTGSKAEQWLT 123
 DB 80 LANFVVGDIIDSDRDKNDF-----AAEVRK-----LRTLFQSLGYD 118
 QY 124 GSPFYIRKI-----LETFTILFAFYLOHYTY-YLPSSAILMGVAQOGLWLIHFAHQ 177
 DB 119 SSKAYTAFKVSFNLGSLTIVAKGQTSITLANVLSAALGLFWQCGWLAHDFLHQ 178
 QY 178 LFKNRYNDLASFYFVGNFQSGGKQHNHVAATNVVGRDGLDLPVFAVAEHL 237
 DB 179 VFQDRFWGLDFAFLGCVGCGFSSSWKDKHNTTHAHPNVHGEDPDIDHPL-LTWSEHA 237
 QY 238 NNYSOD-----SWMTLFRQVHHTF--MLPFLRLSWLLQSIIFV-----SQ 278
 DB 238 LEWSDVPDEELTRMWSRPMVNLQTFYFPLSFARLSWCLQSILFVLPNGOAHKPSGAR 297
 QY 279 MPTHYDIYRNTAIYEOVGLSHWASLGQLY-FLPDWSTRIMFVLSHVLGFLSHVV 337
 DB 298 VP-----ISLVEQLSLAMHWTYLATMELFKDPVNMVLYFLVSAVCGNLLAIF 348
 QY 338 TFNHSYVERKALSSNMSNVACLOIMTTRNMRPGRIDWLWGLNLYQIEHHLPFTMPRN 397
 DB 349 SLNHGMPVISKEEAVDMDFFTKQITGRDVHPGLFANWFTGGLNLYQIEHHLPFTMPRN 408
 QY 398 LNTVMPLKEFAAANGPLVMYDDYFTGFWLEIEQFNRNIANAAKLT 444
 DB 409 FSKIQPAVETLCKKYNRYHTTGMIEGTAEVFSRLNEVSKAASKMGK 455

RESULT 3
 W85121
 ID W85121 standard; peptide: 457 AA.
 DE 11-FEB-1999 (first entry)
 KW Fatty acid; delta-6 desaturase; polyunsaturated fatty acid;
 KW malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis;
 KW cancer; diabetes; eczema; platelet aggregation; vasodilation;
 KW cholesterol level; endometriosis; premenstrual syndrome;
 KW myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;
 KW acute respiratory syndrome; hypertension; inflammatory skin disorder.
 OS Unidentified.
 PN W09846765-A1.
 PD 22-OCT-1998.
 PR 10-APR-1998; U07422.
 PR 11-APR-1997; US-833610.
 PR (ABBO) ABBOTT LAB.
 PA (CALJ) CALGENE LLC.
 PI Chaudhary S, Huang Y, Knutson D, Leonard AE, Mukerji P, Thurmond J.
 DR WPI: 99-009334/01.
 PT New nucleic acid encoding delta5 and other desaturase enzymes .
 PT useful in production of oils of increased arachidonic acid content,
 PT used, e.g. for treating cancer, as foods, animal feeds and cosmetics
 PS disclosure; pages 95-96; 153pp; English.
 CC The present sequence represents a fatty acid delta-6 desaturase enzyme.
 CC The specification describes methods for desaturating a fatty acid and

Q920R9
ID Q920R9 PRELIMINARY; PRT; 444 AA.
AC Q920R9;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE DELTA-6 FATTY ACID DESATURASE.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 95085046.
RA CHO H.P., NAKAMURA M.T., CLARKE S.D.;
RT "Cloning, expression, and nutritional regulation of the mammalian
Delta-6 desaturase."
RL J. Biol. Chem. 274:471-477(1999).
DR EMBL; AF126798; AAD20017.1; -
DR HSSP; P00171; 3B5C.
SQ SEQUENCE 444 AA; 52387 MW; F6F9668B CRC32;

Query Match 18.9%; Score 432; DB 11; Length 444;
Best Local Similarity 28.1%; Pred. No. 4.3e-32;
Matches 121; Conservative 67; Mismatches 182; Indels 60; Gaps 12;
Qy 3 SKRQALSP-----LQMEQTYDVSANVNFHFGGAEIENYQGRDATDA 45
Db 12 TERQAPMPFWEIEIQHNLRDRLVLDKRVYNTKWSQRHGGHRYGHYSGEDATDA 71
Qy 46 ENVMH---FQAEFDKLRMPKINPSFELPPQAAVNEAQEDFRKREELIATCMEDASPL 101
Db 72 FRAHLDLDFVKFLAPLIGELAPEPSLDKQSSQITEDFRALKAKTAEDMNLFTNHL 131
Qy 102 WYSKISTLGLGVLGYFLMVQYQMYF-----ICAVLLGHYQMGWLSHDICHQHT 153
Db 132 FFFELLSHIIVMESLAWFIL---SYEGTGWIPLTATFVLATSAQAGWLQHDYGLSV 197
Qy 154 FNRNWNVGLVFGNGLOGFSVTCWKORHNAHSATNVQGHDPDIDNLPPLAWSDDVT 213
Db 188 YKKSITWNVYHVRFGHGLGASANWNNHRRHFQHKPNIFKDPDKSLHVFVLGEWQPL 247
Qy 214 RASPIRSKLQIQR---QOYFLV-ICILLRFNCFQCVLTVRSUKDRDNQFYRSQYKKEAI 269
Db 248 EYGGKKLLKLPYNHQHEYFELGPPLLIPWFOYQIIMTISRDR----- 293
Qy 270 GLAHLHTLKALFHLF--FMP--SILTSLLVFFVSELVGGFGIAIVVFMNHYPLEKIGDPV 325
Db 293 WYDLAWAISYVMRFYTIYPFYGILGALVFLNFIRLESHWFWVVTQMNLVMEIDLHY 352
Qy 326 WDGHGFSVQIHTNMNIRGIITDWFGLGNTQIEHHLWPTLPRHNLTAVSQVQVEQLCK 385
Db 353 RD--WFS--SOLAATCNVEQSFNDWFSGLHNFQIEHHLFPTMPRHNLHIAIPLVKSICAK 409
Qy 386 HNLVYR-NPL 394
Db 410 HGIEIQERPL 419

RESULT 14
Q92TU8
ID Q92TU8 PRELIMINARY; PRT; 469 AA.
AC Q92TU8;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE S276.
OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
OC Poaceae; Triticum.
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN-CV, ET3;
RA DELHAIZE E., HEBB D.M., GARDNER R.C., RICHARDS K.D.;
RT "Aluminum tolerance in yeast conferred by over-expression of wheat
genes."
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF031194; AAD10250.1; -
DR HSSP; P00171; 3B5C.
DR MENDEL; 35849; Triale; 2419; 35849.
SQ SEQUENCE 469 AA; 52617 MW; E52DB451 CRC32;

Query Match 18.8%; Score 430; DB 10; Length 469;
Best Local Similarity 27.4%; Pred. No. 7.2e-32;
Matches 126; Conservative 68; Mismatches 168; Indels 98; Gaps 15;
Qy 11 LQMEQTYDVSANVNFHFGGAEIENYQGRDATDAFVMVHFOEAFDKLRMPKINP--- 67
Db 46 ISISGDYDVTWLRHHPGGEVPLITLAGODATDAFMAVH-----PPSVRPLLR 95
Qy 67 -----SPELPPQAAVNEAQEDFRKREELIATCMEDASPLWYSKISTLGLGVLGYF 119
Db 96 FVGRLTDTYVPPASA-----DFRRLAQLSSAGLFE-----VGHTPKF 135
Qy 120 LMVQYQMYFQV-----LLGMHYQMGWLSHDICHQHTFKNRNNNL 162
Db 136 LLVAMSVLFCIALYCLACSTGAHMFAGGLIGFIQSGWIGHDSGHQHTIRHPALNRL 195
Qy 163 VGLVFGNGLOGFSVTCWKORHNAHSATNVQGHDPDIDNLPPLA-----WS--EDD 211
Db 196 LQVVSNCILTGLGIAWKNHNTTHLSNLSLHDHDPDLQHLPLFAVSTKFNLSVCYER 255
Qy 212 VTRASPIRSKLQIQQYFELVICILLRFNCFQCV---LTVRSUKDRDNQFYRSQYKKEA 268
Db 256 TLAFDAISFFSVYQHWTFYPMGFARINLLVQSIVELITQKKVRQ-----WLEI 306
Qy 269 IGLAHLHTLKALFHLFMPFSILTSLLVFF--VSELVGGF---GIAVWF-MNHY-PLEKI 321
Db 307 AGVAAFW-----WYPLLVSCLPNMWERVAFLASVITGIVQVFCNLHFSSAVYV 358
Qy 322 GPVMDGHGFSVQIHTNMNIRGIITDWFGLGNTQIEHHLWPTLPRHNLTAVSQVQVEQ 381
Db 359 GPP--KGNDFEFQTAGTLDIKSPWMDWFGHGLQVQVEHLEFPLPRCHRYMVAPIVD 416
Qy 382 LCKKHNLPRNPLPHEGLVILLRYLAVFARMAEKQAPAGKA 421
Db 417 LCKKHGLSYGAATFWEANVTMTKTLRAAALQAREATTGAA 456

RESULT 15
Q92122
ID Q92122 PRELIMINARY; PRT; 444 AA.
AC Q92122;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE DELTA-6 FATTY ACID DESATURASE.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE DAWLEY; TISSUE-LIVER;
RA AKI T., SHIMADA Y., INAGAKI K., HIGASHIMOTO H., KAWAMOTO S.,
RA SHIGETA S., ONO K., SUZUKI O.;
RT "Molecular cloning and functional characterization of rat delta-6
fatty acid desaturase."
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB021980; BAA75496.1; -
DR HSSP; P00171; 3B5C.
SQ SEQUENCE 444 AA; 52380 MW; A5E5B487 CRC32;

```

Query Match      18.88; Score 428.5; DB 11; Length 444;
Best Local Similarity 29.18; Pred. No. 9.2e-32;
Matches 118; Conservative 66; Mismatches 178; Indels 43; Gaps 12;

QY 11 LQLMEQTYDYSAWYFHPGGAETIENVOGRDATDAEVMH---FQEAEDKLRMPKINP 66
Db 37 LVDRKVINVTKWSQRPQGHVIGHYSGEDATDAFAFHLDDLDFVGKFLAPLLIGELAP 96

QY 67 SFELPPOAAVNEAQEDFRKREELIATGCMFDASPLWYSYKISTTLGLGVLYFLMVQYQM 126
Db 97 EEPSLDRGKSQITDEFRAKKTAEEDMNLFTNHLFFLLSHIIVMESIAWFI---S 152

QY 127 YF-----IGAVLLGMHYOQMGWLSHDICHQHTFNRRNNNLVGLVFGNGLOGFSVTC 178
Db 153 YFGNGWIPVTITAFVLATSOAQAGWLOHDYGLSVYKKSINWNIHVHVFVIGHLKASANW 212

QY 179 WKDRHNAHHSATNVQGHDPDIDNLPPLAWSEDDVTRASPISRKLIQF---QOYYFLV-IC 234
Db 213 WNHRRFOHAKPNIFHKDPDIKSLHVFLGEMQPLEYGGKKLKYLPYNHQHEYFFLIGPP 272

QY 235 ILLRFIWCFOCVLTVRSCLKDRDNQFYRSQYKKEAIGLALHWTLK--ALFHLEFMP--SIL 290
Db 273 LLIPMYQYQIIMTM--IRRED-----WDLAWAISYARFFFTYIPFYGIL 317

QY 291 TSLLVFVSELVGGFGIAIVVMNHYPLEKIGDPVWDGCHGFSVQIHTMNIIRGIITDW 350
Db 318 GALVFLNFIRFLESHWFVWVTQMNHIVMEIDLHYRD--WFS-SQLAATCNVEQSFNDW 374

QY 351 FFGGLNYQIEHHLWPTLPRHNLTAVSQVQOLCOKHNLPR-NPL 394
Db 375 FSGHLNFOIEHHLFPTPRHNLHKLAPLVKSLCAKHGIEYOEKPL 419

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